

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2001, 09:41:15 ; Search time 94.04 Seconds

(without alignments)  
2168.100 Million cell updates/sec

Title: US-09-006-352-1

Perfect score: 1077

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/lna/6A.COMB.seq:\*

4: /cgn2\_6/ptodata/2/lna/6B.COMB.seq:\*

5: /cgn2\_6/ptodata/2/lna/PCrUS.COMB.seq:\*

6: /cgn2\_6/ptodata/2/lna/Backfilest1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	129.6	12.0	525	3	US-08-997-918-47
3	112	10.4	2432	3	US-08-974-022-1
4	110.4	10.3	1324	3	US-08-974-022-3
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6	76	7.1	3331	4	US-09-042-785A-1
7	68	6.3	759	4	US-09-042-785A-6
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9	68	6.3	2186	3	US-08-959-382-1
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11	68	6.3	2638	4	US-09-042-785A-22
12	56.4	5.2	1719	4	US-09-042-785A-5
13	54.8	5.1	1164	2	US-08-794-796-1
14	53.8	5.0	1557	1	US-08-385-229-3
15	53.8	5.0	1641	1	US-08-385-229-1
16	53.8	5.0	1641	2	US-08-650-000-1
17	53.8	5.0	1641	6	5395760-1
18	53.8	5.0	2224	4	US-08-477-347-2
19	52.2	4.8	1931	3	US-09-019-942-2
20	52	4.8	2793	1	US-08-209-747-1
21	52	4.8	2793	1	US-08-458-298-1
22	51.6	4.8	3796	2	US-08-762-308-11
23	51.6	4.8	3813	2	US-08-650-000-3
24	51.6	4.8	3813	6	5395760-3
25	49.6	4.6	691	1	US-08-266-080B-12
26	49.6	4.6	691	5	PCR-US95-05423-12
27	49.4	4.6	8906	2	US-08-826-267-1

28	48.6	4.5	1878	3	US-08-996-139-14	Sequence 14, Appl
29	48.6	4.5	1878	4	US-08-995-659-14	Sequence 14, Appl
30	47.8	4.4	3581	2	US-08-738-349-1	Sequence 1, Appl
31	47.2	4.4	1057	1	US-08-147-784-1	Sequence 1, Appl
32	47.2	4.4	1057	4	US-08-195-967-1	Sequence 1, Appl
33	47	4.4	397	3	US-09-253-691-3	Sequence 3, Appl
34	46.6	4.3	543	6	5273901-6	Patent No. 5273901
35	46.6	4.3	1505	2	US-08-909-965C-13	Sequence 13, Appl
36	45.6	4.2	547	1	US-08-131-365B-41	Sequence 41, Appl
37	45.6	4.2	547	2	US-08-668-123-41	Sequence 41, Appl
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39	45.2	4.2	203	4	US-09-043-303-7	Sequence 7, Appl
40	45.2	4.2	1075	4	US-08-400-006B-6	Sequence 6, Appl
41	45.2	4.2	2635	3	US-09-126-280-3	Sequence 3, Appl
42	45.2	4.2	2670	3	US-09-126-280-1	Sequence 1, Appl
43	45.2	4.2	2961	2	US-08-407-875-1	Sequence 1, Appl
44	45	4.2	848	1	US-08-192-480A-1	Sequence 1, Appl
45	45	4.2	1582	3	US-08-545-196B-10	Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-08-794-796-1  
; Sequence 1, Application US/08794796  
; Patent No. 5885800  
; GENERAL INFORMATION:  
; APPLICANT: Emery, John  
; APPLICANT: Tan, KB  
; APPLICANT: Truneh, Alem  
; APPLICANT: Young, Peter  
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
; TITLE OF INVENTION: TR4  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: PastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/794,796  
; FILING DATE: 04-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: GH50000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4026  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1164 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-794-796-1  
Query Match 100.0%; Score 1077; DB 2; Length 1164;



Best Local Similarity 100.0%; Pred. No. 1,7e-209;  
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Db 207 acaccactacccttgcgagcaagcaagcaagcaagcaagcaagcaagcaagcaag 266
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Db 267 ccccaagacacttctgtcagcagcgctgtcgtcgtcgtcgtcgtcgtcgtcgtc 326
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Db 1107 CTATTATTATTAAGCTTTTCATMAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1163

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RESULT: 2
US-08-997-918-47
; Sequence 47, Application us/08997918
; Patent No. 6077689
; GENERAL INFORMATION:
; APPLICANT: Snaveley, Marshall D.
; TITLE OF INVENTION: ENHANCED SOLUBILITY OF RECOMBINANT PROTEINS
; FILE REFERENCE: A-496
; CURRENT APPLICATION NUMBER: US/08/997,918
; CURRENT FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentlin Ver. 2.1
; SEQ ID NO 47
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-08-997-918-47

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Query Match 12.0%; Score 129.6; DB 3; Length 525;  
Best Local Similarity 53.6%; Pred. No. 4.9e-18;  
Matches 270; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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OY 182 ccccaagcacttctgtcagcagcagcagcagcagcagcagcagcagcagcagc 241
Db 74 ctccggtactctccgaaacagcagcagcagcagcagcagcagcagcagcagcagc 133
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Db 314 cgcctgttctcgttctcgtcagcgtcgtcagcgtcgtcagcgtcgtcagcgtcgtc 373
OY 482 gcccccagcagcactctctcagcagcagcagcagcagcagcagcagcagcagcagc 541
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RESULT 3  
US-08-974-022-1  
; Sequence 1, Application us/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.







QY 442 gccgcgagcaccgcccaagcgcgaagaacagcagcagcagccgagccccccagcactctca 501  
Db 483 CAACCTGGAAACCCAGAGCGCAAAACACAGTTTGGCAAAAAATGTCCAGATGGGTCTCTCA 542E

QY 502 gccagcagcctccagcctcagagcagctgcacagcccccagccagcactgcagagccctggagctg 561  
Db 543 GGTGAGACTTTATGTGAAAGACACCTGTTATMAAACACAGACACTGACACATTTGGGCTC 602E

QY 562 gccctcaatgtgcagagctcttctctccaaigacacacccctgfacacagctgca 613  
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2      US-08-974-022-5
3      Sequence 5, Application US/08974022
4      Patent No. 6015938
5      GENERAL INFORMATION:
6      APPLICANT: Boyle, William J.
7      APPLICANT: Lacey, David L.
8      APPLICANT: Calzone, Frank J.
9      APPLICANT: Chang, Ming-Shi
10     TITLE OF INVENTION: OSTEOPROTEGERIN
11     NUMBER OF SEQUENCES: 53
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: Amgen Inc.
14     STREET: 1840 Dehavilland Drive
15     CITY: Thousand Oaks
16     STATE: California
17     COUNTRY: USA
18     ZIP: 91320-1789
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: Patent In Release #1.0, Version #1.30
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/08/974,022
26     FILING DATE: 12-DEC-1995
27     CLASSIFICATION:
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: 08/577,788
30     FILING DATE:
31     ATTORNEY/AGENT INFORMATION:
32     NAME: Winter, Robert B.
33     REFERENCE/DOCKET NUMBER: A-378
34     INFORMATION FOR SEQ. ID NO.: 5:
35     SEQUENCE CHARACTERISTICS:
36     LENGTH: 1135 base pairs
37     TYPE: nucleic acid
38     STRANDEDNESS: single
39     TOPOLOGY: linear
40     MOLECULE TYPE: cDNA
41     FEATURE:
42     NAME/KEY: CDS
43     LOCATION: 94..1296
44     US-08-974-022-5

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Db	227	CTCTGTGTACTTACTTAAACAAACACTGTATACGCAAAAGTGAAGAACCTGTGCGCCCTT	286
QY	242	gtccacgcgcgacctaaagcagagttcttgcgaacttaccctggagcgctgtcgctactgtcaag	301

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Qy	302	tccctctcggggagacgcygagagagagcaaggagctctgcagcgccagccacacacacgctgcct	361
Db	347	CCGTCTCGAAGGACCTCCAGTACTCAAGCAGAGCTCCATTCGACCCACCAACCGCTGT	406
Qy	362	gcgcgtccgcagcagcgtctcttcgcgagcgtgtctctctcttggagagacgactcgtgtc	421
Db	407	GCGAATCGAACGAGGGCGCGCTACTTTAGATAGAGTTCTCTTGAACATAGGAGCTGCC	466
Qy	422	cactctcttgcggagctgattatgcgcccggagaccccccagcagaacagcagctgcagcgt	481
Db	467	CTCTCGATTTTGGAGTGGTGTCGACAGCTGGAAACCCAGACGCAATACAGTTTGCMAAAGAT	526
Qy	482	ggcccaccagagcactctctagccagcagctccagctctagagcagctgcagcccccagca	541
Db	527	GTCACAGATGGTTTCTTCTCAATGACAGCTCATATCTAAAGCAACCTGTGAGAAATACACAA	586
Qy	542	actctgaaggccctcggcctcctcgaacctcaatgtgccagcctctctcccatgacacctgt	601
Db	587	ATTGCACTGTTTGTGGTCTCTGCTTACTCAGAAAGAAATGCAACACGACGACACATAT	646
Qy	602	gcaccagctcagctg	616
Db	647	GTTCCGGAAACAGTG	661

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1      RESULT        6
2      US-09-042-785A-1
3      : Sequence 1, Application US/09042785A
4      : Patent No. 6194151
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Busfield, Samantha J
8      : TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
9      : TITLE OF INVENTION: AND USES THEREFOR
10     : NUMBER OF INVENTIONS: 31
11     : NUMBER OF SEQUENCES: 31
12     : CORRESPONDENCE ADDRESS:
13     : ADDRESSEE: LAHIVE & COCKFIELD, LLP
14     : STREET: 28 State Street
15     : City: Boston
16     : STATE: Massachusetts
17     : COUNTRY: USA
18     : ZIP: 02109
19     :
20     : COMPUTER READABLE FORM:
21     : MEDIUM TYPE: Floppy disk
22     : COMPUTER: IBM PC compatible
23     : OPERATING SYSTEM: PC-DOS/MS-DOS
24     : SOFTWARE: Patent Release #1.0, Version #1.25
25     : CURRENT APPLICATION NUMBER: US/09/042,785A
26     : FILING DATE: 17-MAR-1998
27     : PRIORITY APPLICATION DATA:
28     : APPLICATION NUMBER: US 08/938,896
29     : FILING DATE: 26-SEP-1997
30     : ATTORNEY/AGENT INFORMATION:
31     : NAME: Mandragouras, Amy E
32     : REGISTRATION NUMBER: 36,207
33     : REFERENCE/DOCKET NUMBER: MEI-001CP
34     : TELECOMMUNICATION INFORMATION:
35     : TELEPHONE: (617)227-7400
36     : TELEFAX: (617)742-4214
37     : INFORMATION FOR SEQ ID NO: 1:
38     : SEQUENCE CHARACTERISTICS:
39     : LENGTH: 331 base pairs
40     : TYPE: nucleic acid
41     : STRANDEDNESS: single
42     : TOPOLOGY: linear
43     : MOLECULE TYPE: cDNA
44     : FEATURE:
45     : NAME/KEY: CDS
46     : LOCATION: 344..2065
47     : US-09-042-785A-1

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: November 2, 2001, 13:30:49 ; Search time 39.52 Seconds

(with alignments)  
3880.112 Million cell updates/sec

Title: US-09-006-352-1\_COPY\_115\_924

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	810	100.0	1164	2	US-08-794-796-1 Sequence 1, Appl
2	129.6	16.0	525	3	US-08-997-918-47 Sequence 47, Appl
3	112	13.8	2432	3	US-08-974-022-1 Sequence 1, Appl
4	110.4	13.6	1324	3	US-08-974-022-3 Sequence 3, Appl
5	103	12.7	1355	3	US-08-974-022-5 Sequence 5, Appl
6	76	9.4	3331	4	US-09-042-785A-1 Sequence 1, Appl
7	68	8.4	759	4	US-09-042-785A-6 Sequence 6, Appl
8	68	8.4	1815	4	US-09-042-785A-24 Sequence 24, Appl
9	68	8.4	2186	3	US-08-959-382-1 Sequence 1, Appl
10	68	8.4	2612	4	US-09-042-785A-3 Sequence 3, Appl
11	68	8.4	2638	4	US-09-042-785A-22 Sequence 22, Appl
12	56.4	7.0	1719	4	US-09-042-785A-5 Sequence 5, Appl
13	54.8	6.8	1164	2	US-08-794-796-1 Sequence 1, Appl
14	52	6.4	2793	1	US-08-209-747-1 Sequence 1, Appl
15	52	6.4	2793	1	US-08-458-298-1 Sequence 1, Appl
16	51.6	6.4	3796	2	US-08-762-308-11 Sequence 11, Appl
17	51.6	6.4	3813	2	US-08-650-000-3 Sequence 3, Appl
18	51.6	6.4	3813	6	5395760-3 Patent No. 5395760
19	49.6	6.1	691	1	US-08-266-0808-12 Sequence 12, Appl
20	49.6	6.1	691	1	PCUT-US95-05423-12 Sequence 12, Appl
21	49.4	6.1	8906	2	US-08-826-267-1 Sequence 1, Appl
22	48.6	6.0	1878	3	US-08-996-139-14 Sequence 14, Appl
23	48.6	6.0	1878	4	US-08-995-659-14 Sequence 14, Appl
24	48	5.9	1557	1	US-08-385-229-3 Sequence 3, Appl
25	48	5.9	1641	1	US-08-385-229-1 Sequence 1, Appl
26	48	5.9	1641	2	US-08-650-000-1 Sequence 1, Appl
27	48	5.9	1641	6	5395760-1 Patent No. 5395760

28	48	5.9	2224	4	US-08-477-347-2 Sequence 2, Appl
29	47	5.8	397	3	US-09-253-691-3 Sequence 3, Appl
30	46.6	5.8	543	6	5273901-6 Patent No. 5273901
31	45.4	5.6	1057	4	US-08-147-784-1 Sequence 1, Appl
32	45.4	5.6	1057	4	US-08-195-967-1 Sequence 1, Appl
33	45.2	5.6	203	4	US-09-043-303-7 Sequence 7, Appl
34	45.2	5.6	2635	3	US-09-126-280-3 Sequence 3, Appl
35	45.2	5.6	2670	3	US-09-126-280-1 Sequence 1, Appl
36	45.2	5.6	2961	2	US-08-602-791-1 Sequence 1, Appl
37	44.4	5.5	1600	3	US-08-407-875-1 Sequence 1, Appl
38	44.4	5.5	3386	4	US-09-041-886-1 Sequence 1, Appl
39	44.4	5.4	2580	3	US-09-050-863-2 Sequence 2, Appl
40	44	5.4	3452	2	US-09-130-114-1 Sequence 1, Appl
41	44	5.4	9600	4	US-08-910-647-1 Sequence 1, Appl
42	44	5.4	10596	1	US-07-884-811-15 Sequence 15, Appl
43	44	5.4	10596	1	US-07-885-971-15 Sequence 15, Appl
44	44	5.4	10596	1	US-08-087-783A-15 Sequence 15, Appl
45	44	5.4	10596	1	US-08-194-088B-15 Sequence 15, Appl

#### ALIGNMENTS

RESULT 1  
US-08-794-796-1  
Sequence 1, Application US/08794796  
Patent No. 5885800  
GENERAL INFORMATION:  
APPLICANT: Emery, John  
APPLICANT: Tan, KB  
APPLICANT: Truneh, Alem  
APPLICANT: Young, Peter  
TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794, 796  
FILING DATE: 04-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Han, William T  
REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: GH50000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5219  
TELEFAX: 610-270-4026  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1164 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-794-796-1

Query Match 100.0%; Score 810; DB 2; Length 1164;



Best Local Similarity 100.0%; Pred. No. 5.6e-150;  
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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:   LENGTH: 525
:   TYPE: DNA
:   ORGANISM: Artificial Sequence
:   FEATURE:
:   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
:   OTHER INFORMATION: Fragment encoding amino acids 22-194 of human OPO
:   OS-08-957-918-47

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Query Match	16.0%;	Score 129.6;	DB 3;	Length 525;
Best Local Similarity	53.6%;	Pred. No. 1.7e-17;		
Matches 270; Conservative	0;	Mismatches 234;	Indels 0;	Gaps 0

[illegible]

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RESULT      2
US-08-997-918-47
: Sequence 47, Application US/08997918
: Patent No. 6077689
:
: GENERAL INFORMATION:
: APPLICANT: Snavely, Marshall D.
: TITLE OF INVENTION: ENHANCED SOLUBILITY OF RECOMBINANT PROTEINS
: FILE REFERENCE: A-496
: CURRENT APPLICATION NUMBER: US/08/997,918
: CURRENT FILING DATE: 1997-12-24
: NUMBER OF SEQ ID NOS: 59
: SOFTWARE: Patentin Ver. 2.1
:
: SEQ ID NO 47

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RESULT 3  
 US-08-974-022-1  
 : Sequence 1, Application US/08974022  
 : Patent No. 6015938  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Boyle, William J.  
 : APPLICANT: Lacey, David L.  
 : APPLICANT: Calzone, Frank J.  
 : APPLICANT: Chang, Ming-Shi  
 : TITLE OF INVENTION: OSTROPROTEGERIN  
 :  
 : NUMBER OF SEQUENCES: 53  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESS: Angen Inc.  
 : STREET: 1840 Delavalland Drive  
 : CITY: Thousand Oaks  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 91320-1789  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBA PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30







Patent No 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1355 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 94..1296  
US-08-974-022-5

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Db	527 GTCCAGATGGGTTCTTTCACAAATGAGACGTCATCTTAAAGACCCCTGTGAAAAACACAGAA	588
Qy	428 atcgacagccctctggcctctgacgctcaatgtgcagagctctcccccataagacccctgc	487
Db	587 ATTGCAGTCTCTTTTGGTCTCCTGCTAACTCAGAAAGAAATGCAACACACGCAACATAT	646
Qy	488 gcacacagctgcaatc 502	
Db	647 GTTCGGAAGACAGTG 661	

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RESULT 6
US-09-042-785A-1
Sequence 1, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 344..2065
US-09-042-785A-1

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Db	167	CTCCAAAGTACCTTCATMTATGACGAAGAAGAACTCTCATCACTGTTTGTGACAAATGTC	226		
Qy	68	ccccagagcaactctgtgtgcagcgccgctgtgcgcgagaaagccccaagcgtgtgtgccgt	127		
Db	227	CTCTCTGGTACTTACCTTAATACAAACTGTACAGCAAAATGGAAAGACCGTGTGGCCCTT	286		
Qy	128	gtccacccgcgcacactacacgcagctctcgtgaactctggaaatctggagcgctgtcgactactgaacg	187		
Db	287	GCCTTGACCACTMTATACAGACAGACACTGTGGCAACCAAGTACAGAGACTGTCTTATACGACGC	346		
Qy	188	tctcttgcgagagagcgcttgagagagagagagcagggcttgcgacgcgcccacccaacacgctgtcct	247		
Db	347	CCCTGTGTCAAGAGAGCTGCAGTACGTCACAGCAGAGATGCAATTCGACCCACCAACCCGGGTG	406		
Qy	248	gcccgttcgcgcacacggctctctctgcgcacgcgctgtgttctgtcttggagacgcagcatctgtatc	307		
Db	407	GCGAATGTCAAGGAAGGGCGCTTACTTGAGATGTAGAGTTCTGTTAAMCAATGAGAGCTGCC	466		
Qy	308	cactctgttgccggcgatgattccccggggacacccccagcagaaagacagcatgtgcagcgct	367		
Db	467	CTCTCTGATTTGGAGTGTGCAAGCTGTGACACCCAGAGACGAATATACAGTTTGCAAAAAGAT	526		
Qy	368	gccccccaggaactctctcagccagcagctccagctcagagcagatgtgcagcccccacgca	427		

Query Match	100%	Score	76	DB	4	Length	3331
Best Local Similarity	46.9%	Pred.	No. 5,36-07				
Matches	228	Conservative	0	Mismatches	270	Indels	0
							Gaps
							0







Mon Nov 5 08:22:37 2001

us-09-006-352-1\_copy\_115\_924.rni

Page 6

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? TELEPHONE: (617)227-7400
? TELEFAX: (617)742-4214
? INFORMATION FOR SEQ ID NO: 24:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1815 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
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? MOLECULE TYPE: cDNA
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? NAME/KEY: CDS
? LOCATION: 1..1815
? OS-09-042-785A-24

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Query Match 8.4%; Score 68; DB 4; Length 1815;  
Best Local Similarity 45.9%; Pred. NO. 1.8e-05;  
Matches 233; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

OY	12	caactacccccctggcgaggagcaagaagaacaggagacgcgtgtgtgtgcgcccagatgcctccc	71
Db	156	CACATACCGGCATTTGACCCGTGCACCGCGCAGAGTCTAAACCTGTGACAAGTGTCCAGC	21.5
OY	72	aggacaccttctgtgagcgcgctgtgcgcgagaaagccccaacgaacgtgtgtcccggtgtgc	13.11
Db	216	AGGAACCTATGTCTCTAGCATTTCTTACCACACAAAGCTCTCGGCTCTGCACACACTTGC	27.5
OY	132	accgcgcgcacacacgcgaagttcttgaaactaccttgaaagcgtgcgcgtcacttgaagactct	19.1
Db	276	TGTGTGGACCTTTACCAACCCATGACATATGCGATGAGACAAATGCCATATACCTGTACTCGAC	33.5
OY	192	ctcgcgcggagagctgtgagagagagacagggcttgcacagcccaacacacgtgtcgtgcg	25.1
Db	336	ATGCCCCATGGCCATATGATTTGAATAATTACTTTGTGCTGCTCTGTGACTAGCAGAGATGCAC	38.5
OY	252	ctgcgcgcacgcggtcttcttcgcgcacgcgtgtgttctgtctgttgagacgaacgtgtgtccac	31.11
Db	396	TTTGCCCACTGTGCAATGTGTCTACATCTTAACGGCTACTCTGTGCCCCCATATGCGGTGTCTGT	45.5
OY	312	tgtgtgcgcgagtgatgtgcgcccgagcaaccccaacagaaacacgcagtgccagccgltgc	37.11
Db	456	GGGTTGGGGTGTGGCGAAGAAAGGGAAGAGACTGAGGAGATGTGGGGTGAAGCAAGTGTGC	51.5
OY	372	ccccagcaactctctcaagccagacagctcccaagctcagagagagtgccagccccaccgcgcaactg	43.11
Db	516	TGGGGGTACTCTTCTCAATATGTGCTTCTTAAGTGTATATAAATGCAAAACATATCACACAGCTG	57.5
OY	432	caagcgcctgtgagcctgtgcacctcaatgtgcagagctcttccctccattgacacccctgtgcac	49.1
Db	576	TCTTAGTATGAAGACTGTGTGTGTATCAAGCCGGGGGACCAAGAGACAGACAAAGCTTGTGG	63.5
OY	492	caagctgcaactgtgcttcccccctcaagacac	51.9
Db	636	CACACTCCCGCTCTTCTTCACAGCTCTGCAC	66.3

RESULT 9  
US-08-959-382-1  
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1 COUNTRY: USA
2 ZIP: 19482
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Diskette
5 COMPUTER: IBM Compatible
6 OPERATING SYSTEM: DOS
7 SOFTWARE: FAST-SEO for Windows Version 2.0
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/959,382
10 FILING DATE: 28-OCT-1997
11 CLASSIFICATION: 514
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: 60/041,796
14 FILING DATE: 02-APR-1997
15 ATTORNEY/AGENT INFORMATION:
16 NAME: PRESTIA, PAUL F
17 REGISTRATION NUMBER: 23,031
18 REFERENCE/DOCKET NUMBER: GH-50017
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 610-407-0700
21 TELEFAX: 610-407-0701
22 TELEX: 846169
23 INFORMATION FOR SEQ ID NO: 1:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 2166 base pairs
26 TYPE: nucleic acid
27 STRANDEDNESS: single
28 TOPOLOGY: linear
29 MOLECULE TYPE: CDNA
30 US-08-959-382-1

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Query Match 8.4%; Score 68; DB 3; Length 2186;  
Best Local Similarity 45.9%; Pred. No. 1.9e-05;  
Matches 233; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

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APPLICATION NUMBER: US/08/458,298  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,747  
FILING DATE: 14-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1447-104P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2793 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Nephila clavipes  
TISSUE TYPE: minor ampullate gland  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 183..2675  
OTHER INFORMATION: /product= "N. clavipes minor  
OTHER INFORMATION: ampullate silk protein"  
US-08-458-298-1

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Best Local Similarity 51.8%; Pred. No. 0.025;  
Matches 118; Conservative 0; Mismatches 110; Indels 0; Gaps 0;  
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QY 613 gccctcagagcccgagaggtgtggtgcgacacaaagggccgagcgcttcag 672  
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QY 673 ctgaagctgagctgagctcaaggaatctctgggggagcgagagcgagcgctgtg 732  
DB 1875 CAGCTGCTGAGCAGAGCTGAGGCGCTGCGGATTACAGTACAGAGTGTGCTG 1934  
QY 733 cggctgtcagagcgctgcgctgagcagatgcccgggctggagcgg 780  
DB 1935 CCGCTGTGCTGAGCTGAGCGCTGACAGTGCAGAGCAGAGAGCTG 1982

Search completed: November 2, 2001, 15:03:58  
Job time: 5589 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2001, 12:34:01 ; Search time 13.94 Seconds

(without alignments)  
443.121 Million cell updates/sec

Title: US-09-006-352-2

Perfect score: 1634  
Sequence: 1 MRALGPGLSLCLVLALPA.....RVARMPGLERSVERFLFVH 300

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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5: /cgn2\_6/prodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634	100.0	300	2	US-08-794-796-2
2	444	27.2	401	3	US-08-974-022-6
3	444	27.2	401	4	US-09-042-785A-12
4	425.5	26.0	401	3	US-08-974-022-2
5	424.5	26.0	401	3	US-08-974-022-2
6	424.5	26.0	401	4	US-09-042-785A-13
7	353.5	21.6	461	4	US-09-042-785A-13
8	351.5	21.5	461	1	US-08-385-229-2
9	351.5	21.5	461	2	US-08-650-000-2
10	351.5	21.5	461	4	US-08-477-347-3
11	351.5	21.5	461	6	5395760-2
12	346	21.2	227	3	US-08-974-022-48
13	344	21.1	486	1	US-08-243-010-1
14	344	21.1	518	1	US-08-385-229-4
15	332.5	20.3	474	2	US-08-650-000-4
16	332.5	20.3	474	4	US-09-042-785A-8
17	332.5	20.3	474	6	5395760-4
18	318	19.5	163	4	US-08-219-237B-5
19	318	19.5	163	4	US-08-477-347-13
20	316	19.3	164	2	US-08-232-087A-9
21	287	17.6	605	4	US-09-042-785A-4
22	287	17.6	605	4	US-09-042-785A-23
23	287	17.6	655	3	US-08-959-382-2
24	285.5	17.5	197	2	US-08-505-606-1
25	264.5	16.2	355	1	US-08-292-549-6
26	246	15.1	283	3	PCT-US86-12374-2
27	239	14.6	451	3	US-08-996-139-4

28	239	14.6	451	4	US-08-995-659-4	Sequence 4, App11
29	239	14.6	616	3	US-08-996-139-6	Sequence 6, App11
30	239	14.6	616	4	US-08-995-659-6	Sequence 6, App11
31	236.5	14.5	207	3	US-08-974-022-47	Sequence 47, App1
32	236.5	14.5	325	4	US-08-292-549-2	Sequence 2, App11
33	236.5	14.5	325	4	US-09-042-785A-9	Sequence 9, App11
34	236.5	14.5	325	5	PCT-US91-02207-2	Sequence 2, App11
35	235.5	14.4	591	4	US-08-995-659-2	Sequence 2, App11
36	235.5	14.4	591	4	US-08-995-659-2	Sequence 2, App11
37	233.5	14.3	625	3	US-08-996-139-15	Sequence 15, App1
38	233.5	14.3	625	4	US-08-995-659-15	Sequence 15, App1
39	226	13.8	277	2	US-08-147-784-2	Sequence 2, App11
40	226	13.8	277	4	US-08-195-967-2	Sequence 2, App11
41	225	13.8	573	4	US-09-042-785A-2	Sequence 2, App11
42	215	13.2	326	1	US-08-292-549-4	Sequence 4, App11
43	215	13.2	326	5	PCT-US91-02207-4	Sequence 4, App11
44	214	13.1	205	3	US-08-974-022-51	Sequence 51, App1
45	212	13.0	139	2	US-08-219-237B-8	Sequence 8, App11

## ALIGNMENTS

RESULT 1  
US-08-794-796-2  
; Sequence 2, Application US/08794796  
; Patent No. 5885800  
GENERAL INFORMATION:  
APPLICANT: Emery, John  
APPLICANT: Tan, KB  
APPLICANT: Young, Alem  
TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
TITLE OF INVENTION: TR4  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794, 796  
FILING DATE: 04-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Han, William T  
REGISTRATION NUMBER: 34,344  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5219  
TELEFAX: 610-270-4026  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-794-796-2  
Query Match 100.0%; Score 1634; DB 2; Length 300;



Best Local Similarity 100.0%; Pred. No. 1.8e-127;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALGPGSLICLVLPALPVPVAVGVAET-PTYPWRDAETGERLVCAOCPPGTFFVOR 60  
1 MRALGPGSLICLVLPALPVPVAVGVAET-PTYPWRDAETGERLVCAOCPPGTFFVOR 60  
Db 1 MRALGPGSLICLVLPALPVPVAVGVAET-PTYPWRDAETGERLVCAOCPPGTFFVOR 60  
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61 PCRRDPTGCPGPPRRHYTOFWMYLERCRVCNVLGGEREBARACHATNHRACRCRTGTF 120  
Db 61 PCRRDPTGCPGPPRRHYTOFWMYLERCRVCNVLGGEREBARACHATNHRACRCRTGTF 120  
QY 121 AHAGFCLEHNASCPGAGVIAFGTPSONTOGCPGPGTFFSASSSSSEOCOPHRNCTALGLA 180  
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Db 121 AHAGFCLEHNASCPGAGVIAFGTPSONTOGCPGPGTFFSASSSSSEOCOPHRNCTALGLA 180  
QY 181 LNVPGSSSHDILCTSCGPFSLTRVPGAECEBAVIDFVAFODISIKRLQALAEAP 240  
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Db 181 LNVPGSSSHDILCTSCGPFSLTRVPGAECEBAVIDFVAFODISIKRLQALAEAP 240  
QY 241 GWGPTPRAGAAQLQIRRLTELLGADGALLVRLQALVAVMPGLERSVREPLPVH 300  
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RESULT 2  
US-08-974-022-6  
Sequence 6, Application US/08974022  
Patent No. 6015938

GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehaviiland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wintler, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-6

Query Match 27.2%; Score 444; DB 3; Length 401;  
Best Local Similarity 39.6%; Pred. No. 3.4e-29;  
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LCLVIALPALPVPVAVGVAET-PTYPWRDAETGERLVCAOCPPGTFFVORCRDPT 68  
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QY 69 TCGCPGPPRRHYTOFWMYLERCRVCNVLGGEREBARACHATNHRACRCRTGTFEHAAGFLE 128  
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QY 129 HASCPCGAGVIAFGTPSONTOGCPGPGTFFSASSSSSEOCOPHRNCTALGLALNVPGSSS 188  
129 HASCPCGAGVIAFGTPSONTOGCPGPGTFFSASSSSSEOCOPHRNCTALGLALNVPGSSS 188  
Db 121 HNSCPGFGVVOAGPFRNTVCKRCPDGFSSNMTSSKAPCRKHTNCSVGLLLTQKNAT 180  
QY 189 HPTICTSCGPFSLTRVPGAE--CERAVIDF 218  
189 HPTICTSCGPFSLTRVPGAE--CERAVIDF 218  
Db 181 HDNI---CGSNSESTQKCGIDVTLCEAFRRF 209

RESULT 3

US-09-042-785A-12  
Sequence 12, Application US/09042785A  
Patent No. 6194151

GENERAL INFORMATION:  
APPLICANT: Busfield, Samantha J  
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,785A  
FILING DATE: 17-MAR-1998  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/938,896  
FILING DATE: 26-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MET-001CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)742-4214  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal  
US-09-042-785A-12

Query Match 27.2%; Score 444; DB 4; Length 401;  
Best Local Similarity 39.6%; Pred. No. 3.4e-29;  
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LCLVIALPALPVPVAVGVAET-PTYPWRDAETGERLVCAOCPPGTFFVORCRDPT 68  
11 LCLVIALPALPVPVAVGVAET-PTYPWRDAETGERLVCAOCPPGTFFVORCRDPT 68  
Db 4 LCLCAL---VFLDISIKMTQETFFPKYLYHDETSKQICDKPCPPGYLKHCHTAKWKT 60  
QY 69 TCGCPGPPRRHYTOFWMYLERCRVCNVLGGEREBARACHATNHRACRCRTGTFEHAAGFLE 128  
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Db 61 VCAPCPDHYTDSMTSDCLCYCSPVCKELQYVKQECNTHNRVCECKEGRLTEIEFCIK 120  
QY 129 HASCPCGAGVIAFGTPSONTOGCPGPGTFFSASSSSSEOCOPHRNCTALGLALNVPGSSS 188  
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1      COUNTRY:  USA
2      ZIP:  02109
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4      COMPUTER READABLE FORM:
5      MEDIUM TYPE:  Floppy disk
6      COMPUTER:  IBM PC compatible
7      OPERATING SYSTEM:  PC-DOS/MS-DOS
8      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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10     CURRENT APPLICATION DATA:
11     APPLICATION NUMBER:  US/09/042,785A
12     FILING DATE:  17 MAR-1998
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14     PRIOR APPLICATION DATA:
15     APPLICATION NUMBER:  US 08/938,896
16     FILING DATE:  26-SEP-1997
17
18     ATTORNEY/AGENT INFORMATION:
19     NAME:  Mandagouras, Amy E
20     REGISTRATION NUMBER:  36,207
21     REFERENCE/DOCKET NUMBER:  MEI-001CP
22     TELECOMMUNICATION INFORMATION:
23     TELEFAX:  (617)742-4214
24     TELEPHONE:  (617)742-7400
25
26     INFORMATION FOR SEQ ID NO:  13:
27     SEQUENCE CHARACTERISTICS:
28     LENGTH:  401 amino acids
29     TYPE:  amino acid
30     TOPOLOGY:  linear
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32     MOLECULE TYPE:  peptide
33     FRAGMENT TYPE:  Internal
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35     US-09-042-785A-13

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APPLICATION NUMBER: US/09/042,785A  
FILING DATE: 17-MAR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/938,896  
FILING DATE: 26-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandiagouras, Amy E  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MEI-001CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 461 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal  
US-09-042-785A-7

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Query Match: 21.6%; Score 353.5; DB 4; Length 461;
Best Local Similarity 29.8%; Pred. No. 1,2e-21;
Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;

QY 8 GLSLTCLVLLPMLPEVPVAVRGVAETPTYPVMDATGE-----RLVCAQCPPE 55
DQ 13 GLELMAAHLPLA-----QVAETPYAP-----EPGSGTLREYDQTOMCKSCSPQ 60
QY 56 TFOVRPCRRNSPTTCGPCPPRHVYTFMVNLEKRCVNLCCGEREEARACHAHNRACRC 115
DQ 61 QHAKVFCTKSTDVCSCEDESTYTQOLMMVNPCLSCSGSCSSDQVETQACTRBQNRICTC 120
QY 116 RTGFFAHAG-----FCLFNASCPPGAGVIAPGTPSONTOCPQCPPTFSASSSSSICQ 169
DQ 121 RPGWYCALSKQEGCRICAPLRKRCRQGFVARNQDTETSDVYCKPCAPQTFNSNTSSDICH 180
QY 170 PHNRCTALGLALNPQSSSHDTLCTSGCGFPLSTFVPGAECECAEYVIDFAQDISIKRL 229
DQ 181 PHQCNVVA----IPGNASRDVACTSTS--PYRSMAPCAVHLPLQPV-----STFSQHT 227
QY 230 QRLLOALEAPE-----GWSPTPERA-----GRAALQKILRRRTITELGADQALIVRLQAL 280
DQ 228 QPPPEPSTASTSFLLPMGSPSPAGSGSDPRLPGLLVGTAL-----GLLIIGVNCV 282
QY 261 ---RVAMP-GLERSYRERFLP 286
DQ 263 IMTVKKKKPLCLQREAKVPHLP 304

RESULT 8
US-08-385-229-2
Sequence 2, Application US/08385229
Patent No. 5605690
GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
TITLE OF INVENTION: Smith, Craig A.
METHOD OF INVENTION: Method of Treating TNF-Dependent
NUMBER OF SEQUENCES: 5
Inflammation Using Tumor Necrosis Factor Antagonists
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patentin Release #1.0 Version #1.25

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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/385,229
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/946,236
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wight, Christopher L.
;; REGISTRATION NUMBER: 31,680
;; REFERENCE/DOCKET NUMBER: 2503
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 587-0430
;; TELEFAX: (206) 587-0606
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 461 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-385-229-2
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Query Match 21.5%; Score 351.5; DB 1; Length 461;
Best Local Similarity 29.8%; Pred. No. 1.7e-21;
Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;
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QY 8 GLSLCLLVLPALPLPVPVAVGVAETPTVPMRDAETGE-----RLVCAOCPG 55
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Db 13 GLELMAAHLPA-----QVAFTPYAP---EPGSTRLEREYDQTAOMCCSKSPG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 56 TVQORPCRDSPPTGCGPCPRHYTOFWNYLERGCYCNVLGGEREEARACHATHNRACRC 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 QHAKVFCTKSDTVDCSCEDSTYTQLNMWVPECLSCGSCSSDQVETQACTRQNRICTC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 RTGFFAHAG-----FCLHASCPPGAGVIAPGTPSONTOCQPCPGTFSASSSSSEQC 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 RPYWCALSKQEGRLCAPLRKCRPGFGVARPGTETSDVYCKPCAPGTFSNTTSSDICTR 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 PHRNCTALGLALNVPSSSHDTLCTGCTGFPPLSTRVPGAECEBRAVDFVAFQDISIKRL 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 PHQICNVVA-----IPGNASMDAVCTSTS--PTSMAPGAVHLQPV-----STRSQHT 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 QRLQLALEPE-----GWCPTPRA---GRAALQKLRRRLTELLGQDQALLVRLQAL 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 QPTPEPSTAPSTFLLPMGSPPEAGSTGDFALPVGLIVGTAL-----GLLIIGVNCV 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 ---RVARMP-GLERSVREPLP 298
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 283 IMQVKKKKPLCLQREAKVPHLP 304
```

```
RESULT 9
US-08-650-000-2
; Sequence 2, Application US/08650000
; Patent No. 5945397
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/650,000
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/468,453
;; FILING DATE:
;; APPLICATION NUMBER: US/08/038,765
;; FILING DATE:
;; APPLICATION NUMBER: US 403,241
;; FILING DATE: 05-SEP-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 405,370
;; FILING DATE: 11-SEP-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 421,417
;; FILING DATE: 13-OCT-1989
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 523,635
;; FILING DATE: 10-MAY-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wight, Christopher L.
;; REGISTRATION NUMBER: 31,680
;; REFERENCE/DOCKET NUMBER: 2501-D
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 587-0430
;; TELEFAX: (206) 233-0644
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 461 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-650-000-2
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Query Match 21.5%; Score 351.5; DB 2; Length 461;
Best Local Similarity 29.8%; Pred. No. 1.7e-21;
Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;
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```
QY 8 GLSLCLLVLPALPLPVPVAVGVAETPTVPMRDAETGE-----RLVCAOCPG 55
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Db 13 GLELMAAHLPA-----QVAFTPYAP---EPGSTRLEREYDQTAOMCCSKSPG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 56 TVQORPCRDSPPTGCGPCPRHYTOFWNYLERGCYCNVLGGEREEARACHATHNRACRC 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 QHAKVFCTKSDTVDCSCEDSTYTQLNMWVPECLSCGSCSSDQVETQACTRQNRICTC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 RTGFFAHAG-----FCLHASCPPGAGVIAPGTPSONTOCQPCPGTFSASSSSSEQC 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 RPYWCALSKQEGRLCAPLRKCRPGFGVARPGTETSDVYCKPCAPGTFSNTTSSDICTR 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 PHRNCTALGLALNVPSSSHDTLCTGCTGFPPLSTRVPGAECEBRAVDFVAFQDISIKRL 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 PHQICNVVA-----IPGNASMDAVCTSTS--PTSMAPGAVHLQPV-----STRSQHT 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 QRLQLALEPE-----GWCPTPRA---GRAALQKLRRRLTELLGQDQALLVRLQAL 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 QPTPEPSTAPSTFLLPMGSPPEAGSTGDFALPVGLIVGTAL-----GLLIIGVNCV 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 ---RVARMP-GLERSVREPLP 298
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 283 IMQVKKKKPLCLQREAKVPHLP 304
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```
RESULT 10
US-08-477-347-3
; Sequence 3, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
```



```

? APPLICANT: BELETSKY, Igor
? APPLICANT: METT, Igor
? TITLE OF INVENTION: TNE LIGANDS
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: BROWDY AND NEIMARK
? STREET: 419 Seventh Street, N.W.
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20004
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/477,347
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/115,685
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: IL 106271
? FILING DATE: 08-JUL-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Townsend, G. Kevin
? REGISTRATION NUMBER: 34,033
? REFERENCE//DOCKET NUMBER: WALLACH-10
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-628-5197
? TELEFAX: 202-737-3528
? TEXT: 248633
? INFORMATION FOR SEQ. ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 461 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-477-347-3

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Query Match      21.5%  Score 351.5;  DB 4;  Length 461;
Best Local Similarity 29.8%;  Pred. No. 1.7e-21;
Matches 96;  Conservative 43;  Mismatches 122;  Indels 61;  Gaps 12;

QY 8 GLSLCLVIALPALLPVAVRGVAETPTYPWRDAETGE-----RLVCAQCPG 55
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 13 GLELMAAALPA-----QVAFTPYAP-----EPGTCRLREYYDOTAQMCCKSPG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 56 TVQVRCRGRDSPITGCRPRHYTOFWNYLERGRYCNVLGGEEREARACHATHNRACRC 115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 QHAKVFCTKTSDFVDCSDSTYTOLMNVPECLSCGRSSSDQVETQACTRQNRICTC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 RTGFEFAHAG-----FCLHASCPRGAGVIAPGPPSONTCQCPGTFSSASSSEDCO 169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 RFGWYCALSKQEGRCIAPLRKCRPGFVGARPGTETSDVYCKRCACGTENSTSDICR 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 PHRNCYALGLALNVPGSSSHDTICTSGTGPLSTRVPGAEECCRAVIDPAFDISIKRL 229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 PHQICNVVA-----IPGNASMDAVCTSTS--PTPSMAPGAVHLQPV-----STRSQHT 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 QRLQLALEAE-----GNGTTPRA-----GRAALQKLRRRLTELGAODGALLVRLQAL 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 QPTPEPSTAPSTSLFLPMGSPSPAEGSTGDFALPVGLIVGTAL-----GLIIGVNCV 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 ---RVARMP-GLERSVREFLP 298
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 IMTVKKRKLCLQREAKVPHLP 304
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```

RESULT 11

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5395760-2
? Patent No. 5395760
? APPLICANT: SMITH, CRAIG A.; GODWIN, RAYMOND G.; BECKMANN,
? M. PATRICIA
? TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
? B-RECEPTORS
? NUMBER OF SEQUENCES: 17
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/523,635
? FILING DATE: 10-MAY-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 421,417
? FILING DATE: 13-OCT-1989
? APPLICATION NUMBER: 405,370
? FILING DATE: 11-SEP-1989
? APPLICATION NUMBER: 403,241
? FILING DATE: 05-SEP-1989
? SEQ. ID NO: 2:
? LENGTH: 461
5395760-2

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Query Match      21.5%  Score 351.5;  DB 6;  Length 461;
Best Local Similarity 29.8%;  Pred. No. 1.7e-21;
Matches 96;  Conservative 43;  Mismatches 122;  Indels 61;  Gaps 12;

QY 8 GLSLCLVIALPALLPVAVRGVAETPTYPWRDAETGE-----RLVCAQCPG 55
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DB 13 GLELMAAALPA-----QVAFTPYAP-----EPGTCRLREYYDOTAQMCCKSPG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 56 TVQVRCRGRDSPITGCRPRHYTOFWNYLERGRYCNVLGGEEREARACHATHNRACRC 115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 QHAKVFCTKTSDFVDCSDSTYTOLMNVPECLSCGRSSSDQVETQACTRQNRICTC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 RTGFEFAHAG-----FCLHASCPRGAGVIAPGPPSONTCQCPGTFSSASSSEDCO 169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 RFGWYCALSKQEGRCIAPLRKCRPGFVGARPGTETSDVYCKRCACGTENSTSDICR 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 PHRNCYALGLALNVPGSSSHDTICTSGTGPLSTRVPGAEECCRAVIDPAFDISIKRL 229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 PHQICNVVA-----IPGNASMDAVCTSTS--PTPSMAPGAVHLQPV-----STRSQHT 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 QRLQLALEAE-----GNGTTPRA-----GRAALQKLRRRLTELGAODGALLVRLQAL 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 QPTPEPSTAPSTSLFLPMGSPSPAEGSTGDFALPVGLIVGTAL-----GLIIGVNCV 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 ---RVARMP-GLERSVREFLP 298
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 IMTVKKRKLCLQREAKVPHLP 304
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```

```

RESULT 12
US-08-974-022-48
? Sequence 48, Application US/08974022
? Patent No. 6015938
? GENERAL INFORMATION:
? APPLICANT: Boyle, William J.
? APPLICANT: Lacey, David L.
? APPLICANT: Calzone, Frank J.
? APPLICANT: Chang, Ming Shi
? TITLE OF INVENTION: OSTEOPROTEGERIN
? NUMBER OF SEQUENCES: 33
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Amgen Inc.
? STREET: 1840 Dehavilland Drive
? CITY: Thousand Oaks
? STATE: California
? COUNTRY: USA
? ZIP: 91320-1789
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS

```







TELEPHONE: (206) 587-0430  
TELEFAX: (206) 587-0606  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 518 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-385-229-4

Query Match 21.1%; Score 344; DB 1; Length 518;  
Best Local Similarity 33.8%; Pred. No. 8e-21;  
Matches 74; Conservative 28; Mismatches 81; Indels 36; Gaps 6;

OY 8 GLSLICLVLPALPYPAVAVGAEPTFYWRDAETGE-----RLVCAACPPG 55  
DB 42 GLELMAAHLPA-----QVAFETYPAP---EPGSTRLREYDQTMCCSKCPG 89  
OY 56 TEVQPCRPDSPTTCGCPRHHTQFWNYLERCRYCNVLCGEREEARACHATHNRACRC 115  
DB 90 QHAKVFCTKSDYVCDSCEDSTYQLNWNVPECLSCGSCSDQVETQACTRREONRICTC 149  
OY 116 RTGFFAHAG-----FLEHASCPGAGVIAFGTSPONTOCOPCPGPTFSASSSSSQOQ 169  
DB 150 RFGVYCALSKOEGRCRLCAPRKCRPGFVARPGTETSDVVCCKPCAPGTFSTSTBICR 209  
OY 170 PHRNCTALGLALNVPSSSHDTLCTSCGTGFPPLSTRVPGA 208  
DB 210 PHQICNVVA---IPGNASMDAVCTSTS--PTRSMAPGA 242

RESULT 15

US-08-650-000-4  
Sequence 4, Application US/08650000  
Patent No. 5945397  
GENERAL INFORMATION:

APPLICANT: Smith, Craig A.  
APPLICANT: Goodwin, Raymond G.  
TITLE OF INVENTION: Tumor Necrosis Factor Receptors  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: U.S.A.  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,000

FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,453  
FILING DATE:  
APPLICATION NUMBER: US/08/038,765  
FILING DATE:  
APPLICATION NUMBER: US 403,241  
FILING DATE: 05-SEP-1989  
PRIOR APPLICATION DATA: US 405,370  
FILING DATE: 11-SEP-1989  
PRIOR APPLICATION DATA: US 421,417  
FILING DATE: 13-OCT-1989  
PRIOR APPLICATION DATA: US 523,635

FILING DATE: 10-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Wright, Christopher L.  
REGISTRATION NUMBER: 31,680  
REFERENCE/DOCKET NUMBER: 2501-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 474 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-650-000-4

Query Match 20.3%; Score 332.5; DB 2; Length 474;  
Best Local Similarity 29.7%; Pred. No. 6.4e-20;  
Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

OY 46 RLVCAACCPOTFVQPCRPDRDPTTCGCPRHHTQFWNYLERCRYCNVLCGEREEARAC 105  
DB 52 QMCCACPCPGQYVYKHCNKTSDTVACADCEASMTQVWNOFRTCLSSSCTDQYEIRAC 111  
OY 106 HATHNRACRCRTGFF---AHAGF---CLEHASCPGAGVIAFGTSPONTOCOPCPGPTF 158  
DB 112 TKOONRVACACAGRYCALKTHSGCRQCRRLSKCPGFCGVASSRAVNGVLCACAPGTF 171  
OY 159 SASSSSSQOQPHRNCTALGLALNVPSSSHDTICT---SCTGFPPLSTRVPGAECERA 214  
DB 172 SDTTSSTDCVCRPHRISILA---IPGNASTDAVCAPESPTLSAIPRTLYSQPEPTRSQ 227  
OY 215 VIDFVAFODISIKRLORLOALEAPGSGPTP---RAGRAIOLKLRRTLLGAD 269  
DB 228 PLD---QERGPGQTSILSL-----GSTPIEDSTGGISLPLGLVGYTSL----- 272  
OY 270 GALLVRLQAL-----RVAKMPGLERSVRRFLP 298  
DB 273 GLMLGLVNCIIIVOKKKRPSCLORDAKVHPV 305

Search completed: October 31, 2001, 12:39:06  
Job time: 305 sec







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[illegible]

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1  APPLICANT: Calzone, Frank J.
2  APPLICANT: Chang, Ming-Shi
3  TITLE OF INVENTION: OSTEOPROTEGERIN
4  NUMBER OF SEQUENCES: 53
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Amgen Inc.
7  STREET: 1840 Dehavenland Drive
8  CITY: Thousand Oaks
9  STATE: California
10 COUNTRY: USA
11 ZIP: 91320-1789
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent In Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/974,022
19 FILING DATE: 12-DEC-1995
20 CLASSIFICATION:
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/577,788
23 FILING DATE:
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Winter, Robert B.
26 REFERENCE/DOCKET NUMBER: A-378
27 INFORMATION FOR SEQ ID NO: 6:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 401 amino acids
30 TYPE: amino acid
31 TOPOLOGY: linear
32 MOLECULE TYPE: protein
33 OS-08-974-022-6

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alignment_scores:
  Quality: 444.00
  Ratio: 3.194
  Percent Similarity: 65.566
  Length: 212
  Gaps: 4
  Percent Identity: 39.623
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alignment_block:
US-09-006-352-1 x US-08-974-022-6 . .
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Align seg 1/1 to: US-08-974-022-6 from: 1 to: 401

[illegible]



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117 eCysLeuYshisArgSerCysProGlyPheGlyValValGlnAla 134
449 GCACCCCGACGACGACGACGACGACGACGACGACGACGACGACGAC 498
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134 LyrhPrGluArgAsnThrValCysLysArgCysProAspLysPhe 150
499 TCAGCCAGCAGCTCCAGCTCCAGCAGCAGCAGCAGCAGCAGCAGC 548
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 SerAsnGluThrSerSerLysAlaProCysArgLysHisThrAsn 167
549 GCGCCCTGGGCTGGCCCTCAATGTGCCAGGCTCTTCCTCCATGAC 598
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seq_documentation_block:
; Sequence 12, Application US/09042785A
; Patient No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-09-042-785a-12

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alignment_scores:
Quality: 444.00      Length: 212
Ratio: 3.194        Gaps: 4
Percent Similarity: 65.566      Percent Identity: 39.623

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alignment_block:
US-09-006-352-1 x US-09-042-785a-12
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; Sequence 2, Application US/08974022
; Patient No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive

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Mon Nov 5 08:22:31 2001

us-09-006-352-1.ra1

Page 4

CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-2

alignment\_scores:  
Quality: 425.50 Length: 205  
Ratio: 3.199 Gaps: 2  
Percent Similarity: 64.878 Percent Identity: 39.512

alignment\_block:  
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Patent No. 6015938

GENERAL INFORMATION:

APPLICANT: Boyle, William J.

APPLICANT: Lacey, David L.

APPLICANT: Calzone, Frank J.

APPLICANT: Chang, Ming-Shi

TITLE OF INVENTION: OSTEOPROTEGERIN

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: 1840 Dehavenland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,022

FILING DATE: 12-DEC-1995

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/577,788

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-378

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 401 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-974-022-4

alignment\_scores:  
Quality: 424.50 Length: 205  
Ratio: 3.144 Gaps: 2  
Percent Similarity: 65.854 Percent Identity: 39.024

alignment\_block:  
US-09-006-352-1 x US-08-974-022-4 ..

Align seg 1/1 to: US-08-974-022-4 from: 1 to: 401

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seq documentation block:
; Sequence 13, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042.785A

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; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-09-042-785A-13

alignment_scores:
    Quality: 424.50      Length: 205
    Ratio: 3.144        Gaps: 2
    Percent Similarity: 65.854    Percent Identity: 39.024

alignment_block:
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424 CCGTGGTGGCGGCTGATGTCGCCCGGCGACCGCCAGACAGCAGTG 473
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seq\_documentation\_block:

Sequence 7, Application US/09042785A  
 Patent No. 6194151  
 GENERAL INFORMATION:  
 APPLICANT: Buxfield, Samantha J  
 TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
 TITLE OF INVENTION: AND USES THEREFOR  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/042,785A  
 FILING DATE: 17-MAR-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/938,896  
 FILING DATE: 26-SEP-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Amy E  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: MEI-001CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)742-4214  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 461 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 US-09-042-785A-7

alignment\_scores:  
 Quality: 357.00 Length: 334  
 Ratio: 1.994 Gaps: 13  
 Percent Similarity: 53.593 Percent Identity: 29.940

alignment\_block:  
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seq\_documentation\_block:

Sequence 2, Application US/08385229  
Patent No. 5605690  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Cindy A.  
TITLE OF INVENTION: Method of Treating TNF-Dependent  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
City: Seattle  
STATE: Washington  
COUNTRY: U.S.A.  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentlin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/385,229  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/946,236  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wright, Christopher L.  
REGISTRATION NUMBER: 31,680  
REFERENCE/DOCKET NUMBER: 2503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 587-0606  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 461 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-385-229-2

alignment\_scores:

Quality: 355.00 Length: 334  
Ratio: 1.994 Gaps: 13  
Percent Similarity: 53.293 Percent Identity: 29.940

alignment\_block:

US-09-006-352-1 x US-08-385-229-2 ..

Align seg 1/1 to: US-08-385-229-2 from: 1 to: 461

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10 GCTCCAGACGACCATGAGCGCTGAGGGCCAGCGCTGCTGCT 59
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
2  AAlaProValAlaValAlaValAlaValAlaValAlaValAla 17
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
60 GTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 109
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
17 PAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 26
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
110 GAGTGGCAGAAACACCACTACCTGCGGAGCAGACGAGGAG 159
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
26 InValAlaPheThrProTyrAlaPro.....GluProLys 38
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
160 .....CGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 173
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

```

39 ThrCysArgLeuArgGluTyrTyrAspGlnThrAlaGlnMetCysCys 55
174 CCAGTGGCCCCCAGGACCTTTGTGACAGGCGGCGCCGAGACACC 223
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
55 rLysCysSerProGlnGlnHisAlaLysValPheCysThrLysThrSera 72
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
224 CCAGACGCTGTGCCCCGTGCCACCGCCGACACTACACGAGTTGTGAA 273
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
72 sPTThrValCysAspSerCysGlnAspSerThrTyrThrGlnLeuTrp 88
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
274 TACCTGGAGCGCTGCCGTACTGACAGCGCTCTGTGCGGGAGACCG 323
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
89 rTrpValProGluCysLeuSerCysGlySerArgCysSerSerAspGln 105
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
324 GGAGCAGCGGCTGTCCAGCCACACCGCCAGCTGCTGCGCTGCCCA 373
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
105 GluThrGlnAlaCysThrArgGlnGlnAsnArgLleCysThrCysArg 122
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
374 CCGGCTCTTCGCGCAGCGTGT.....TTCTGCTTG 405
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
122 roGlyTrpTyrCysAlaLeuSerLysGlnGluCysArgLeuCysAla 138
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
406 GAGCAGCATGCTGTCCACTGTGCGCGCGGTGATGGCCGCGGACCCC 455
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
139 ProLeuArgLysCysArgProGlyPheGlyAlaAlaArgProGlyThr 155
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
456 CAGCCAGAACAGCGTGCAGCGCGTCCGCCCCAGCAGCTCTGAGCA 505
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
155 uThrSerAspValAlaCysLysProCysAlaProGlyThrPheSerAnt 172
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
506 GCAGCTCCAGCTCAGAGCAGTGCACGCCACCCAGCAGACTGCAGCG 555
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
172 hrThrSerSerThrAspLecysArgProHisGlnLleCysAsnValAl 188
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
556 GGCCTGGCCCTCATGTGCGCAGGCTTCTCCATGACACCTGTGCAC 605
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
189 Ala.....IleProLysAsnLaseMetAspAlaValAlaCysTh 201
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
606 CAGCTGACGTGCTCCCTCCAGCACAGGCTTACAGAGTGTAGAGGT 655
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
201 rSerThrSer.....ProThrArgSerMetAlaProGlyAlaValHisL 216
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
656 GTGACGTGCGCCGTCATGACTTGTGCTTCCAGACATCTCCATCAAG 705
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
216 euProGlnProVal.....SerThrArgSerGln 225
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
706 AGCTGACAGCGGCTGTGCGAGCCTCGAGCGCCCGAG..... 744
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
226 HisThrGlnProThrProGlnProSerThrAlaProSerThrSera 242
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
745 ...GGCTGGGCTCGACACCAAGGGCG.....GGCCGCGCG 778
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
242 uLeuProMetGlyProSerProProAlaGluGlySerThrGlyAspPhe 259
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
779 CCTTGACAGTGAAGCTCGCTCGCGCTACACGAGAGCTCTGCGGCGCAG 828
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
259 lAlaProValAlaGlyLeuIleValAlaGlyValThrAlaLeu..... 271
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
829 GACGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 869
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
272 ...GlyLeuLeuIleIleGlyValAlaCysValIleMetThrGlnVal 287
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
870 GGCAGGATGCCCC...GGGCTGAGCGAGGAGCGCTGAGCGCTTCGCC 916
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
287 lLysLysLysProLeuCysLeuGlnArgGlnAlaLysValProHisLeu 304
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
917 CT 918
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304 to 304

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seq\_name: /cgn2\_6/plodata/2/1aa/5B\_COMB.pep:US-08-650-000-2

seq\_documentation\_block:



```

Sequence 2, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:
APPLICATION NUMBER: US 403,241
FILING DATE: 05-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-650-000-2

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Alignment_scores:
Quality: 355.00      Length: 334
Ratio: 1.994        Gaps: 13
Percent Similarity: 53.293      Percent Identity: 29.940

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Alignment\_block:

US-09-006-352-1 x US-08-650-000-2

Align seg 1/1 to: US-08-650-000-2 from: 1 to: 461

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10 GCTCAGCAGAGCATGAGGCGCTGGAGGGCCAGGCGCTGCTGCT 59
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
2 AlaProValAlaValTrrAlaAlaLeu...AlaValGlyLeuGluLeuTr 17
60 GTGCTGTGTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 109
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
17 palaaAlaAlaHisAlaLeuProAla.....G 26

```

```

110 GAGTGGCAAAACACCCCACTACCCCTGGCGGAGCCAGACAGGGAG 159
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
26 InValAlaPheThrProTrrAlaPro.....GluProGlySer 38
160 .....CGGTGGTGGCGC 173
39 ThrCysArgLeuArgGluTrrTyrAspGlnThrAlaGlnMetCysCys 55
174 CCAGTGGCCCCCAGGACACCTTTGTGCAGCGCCGCTGGCGGAGACAG 223
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
55 rlyCysSerProGlyGlnHisAlaLysValPheCysThrTyrSerA 72
224 CCAGCAGCTGTGCCCGCTGCCACCCGCCACATACAGCAGCATTTGGA 273
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
72 sPlrrValCysAspSerCysGluAspSerThrTrrGlnLeuTrrAsn 88
274 TACCTGAGAGCGCTGCGCTACTGCAAGCTGCTGCGGAGAGCGTGA 323
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
89 TrpAlProGluCysLeuSerCysGlySerArgCysSerSerAspGln 105
324 GGAGCAGAGGCTTGGCCAGCCACACCAACCGCTGCGCGCGCGCA 373
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
105 lGluThrGlnAlaCysThrArgGluGlnAsnArgIleCysThrCysArg 122
374 CGGCTGCTGGCGCCAGCGCTGCT.....TTCGTGTG 405
122 roGlyTrrTrrCysAlaLeuSerIlyGlnGluCysArgLeuCysAla 138
406 GAGCAGCATGCTGTCCACCTGTGTCGGCGCTGATGGCCCGGACACC 455
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
139 ProLeuArgIlyCysArgProGlyPheIlyAlaAlaArgProGlyThr 155
456 CAGCCAGAACAGCAGTGCAGCGCTGCCCGCCAGGACCTTCTCAGCA 505
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
155 uThrSerAspValValCysIlySProCysAlaProGlyThrPheSerAsn 172
506 GCAGCTCAGCTCAGAGCAGTGCAGCCGCCACCGCACTGCAGCGCCCT 555
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
172 hrrThrSerThrAspIleCysArgProHisGlnIleCysAsnValVal 188
556 GAGCTGGCCCTCAATGTGCAGGCTTCTCCCATACACCGCTGTGCAC 605
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
189 Ala.....IleProGlyAsnAlaSerMetAspAlaValCysThr 201
606 CAGCTGACAGTGGTCCCTCCCTCAGCAGGAGGTACAGGAGCTGAGAGT 655
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
201 rSerThrSer.....ProThrArgSerMetAlaProGlyAlaValHisL 216
656 GTGAGCGGTGCGCTCATGAGCTTGTGGCTTCCAGGACATGTCATCAG 705
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
216 euProGlnProVal.....SerThrArgSerGln 225
706 AGGCTGCAGCGCTGCTGCAGCCCTGAGGCCCGCCGAG..... 744
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
226 HisThrGlnProThrProGluProSerThrAlaProSerThrSerPhe 242
745 .....GGCTGGGCTCGACACCAAGGCG.....GGCCGCGCG 778
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
242 uLeuProMetIlyProSerProAlaGluGlySerThrIlyAspPheA 259
779 CTTTGACAGCTGAAGCTGCTGCGCGCTCAGGAGCTTCGTGGCGCGCAG 828
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
259 lAlaProValIlyLeuIleValAlaIlyAlaThrAlaLeu..... 271
829 GACGGGGCGCTGTGTGGCGCTGCTGCAGGCGCTG.....CGCGT 869
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
272 ..GlyLeuLeuIleIleGlyValValAsnGlyValIleMetThrGln 287
870 GAGCAGATGCGC...GGGCTGGAGCGAGGCGCTGAGCGGCTTCTCTCC 916
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
287 llySlyIlySProLeuCysLeuGlnArgGluAlaIlyValProHisLeu 304

```















```

46 pAlaAlaAlaAlaLeuProAla.....G 55
110 GAGTGGCAGAAACACCCACCTTACCCCTGGCGGGAGCAGAGAGAGGAG 159
55 InValAlaAlaAlaPro.....GluProGlySer 67
160 .....CGCTGGTGGTGGC 173
68 ThrCysArgLeuArgGluTyrTyrAspGlnThrAlaGlnMetCysCysSe 84
174 CCAGTGGCCCCCAGCAGCCTTTGTGACGGCGCTGGCCGCGAGACACC 223
84 rlyscYssrProGlyGlnHisAlaValPheCysThrLysThrSerA 101
224 CCAGCAGCTGTGGCCCGCTGTCACCGCCGCTACACGACCTTGTGAAC 273
101 spThrValCysAspSerCysGluAspSerThrTyrThrGlnLeuTrpAsn 117
274 TACCTGGAGCGCTGGCGCTACTGCAACGCTCTCTGCGGGAGACCTGAGA 323
118 TrpValProGlyCysLeuSerCysGlySerArgCysSerAspGlnVa 134
324 GGAGCAGCGGCTTGGCAGCCACCCACACACCGTGGCTGGCGCTGGCA 373
134 lAluThrGlnAlaCysThrArgGlnGlnAsnArgIleCysThrCysArgP 151
374 CCGGCTTCTTGGCAGCTGGT.....TTCTGCTTG 405
151 roGlyTrpTyrCysAlaLeuSerLysGlnGluGlyCysArgLeuCysAla 167
406 GAGCAGCATCTGTCACCTGATGCGCGCTGATGCGCGCGAGCAGCC 455
168 ProLeuArgLysCysArgProGlyPheGlyAlaAlaArgProGlyThrOl 184
456 CAGCCAGAACACGAGTGGCAGCGCTGCGCCCGCAGCAGCCTTCTGAGCA 505
184 uThrSerAspValAlaCysLysProCysAlaProGlyThrPheSerAnt 201
506 GCAGCTCCAGCTCAGAGCAGTCCAGCCACCGCAGCAGCTGAGCGCCG 555
201 hThrSerSerThrAspIleCysArgProHisGlnIleCysAsnValAla 217
556 GGCCTGGCCCTCAATGTGCGCAGGCTCTCTCCATGACACCCCTGTGAC 605
218 Ala.....lleProGlyAsnAlaSerMetAspAlaValCysTh 230
606 CAGCTGCACTGGCTTCCCTCAGACAGGAGTACAGAGGTGAGAGT 655
230 rSerThrSer.....ProThrArgSerMetAlaProGlyAlaValHisL 245
656 GTGAGCGTCCCGTCATCGACTTGTGGCT..... 685
245 euProGln..ProValSerThrArgSerGlnHisThrGlnProThrProGl 261
686 TCCAGGACATCTCCATCAAGAGGCTGACAGCGGCTGACAGCCCTGCA 734
261 uProSerThrAlaProSerThrSerPheLeuLeuPrometGlyProSerP 278
735 GGCCCGGAGGAGGTGGGTCCGACACACAGAGGAGCGCGCGCGCTTGC 784
278 roProAlaGluGlySerThr.....GlyAspGluProLysSerCys 291
785 ACCTCAAGTGTGCGCGGCTCAGCAGACCTCTGGGGGCGCAGAGCAGG 834
292 Asp.....LysThrHis 295
835 GCGCTGCTGTGCGGTGTGTCAGAGCGGTGCGGTGCGCAGAGTACCCGG 884
295 sThrCys.....ProProCysPro. 301
885 GCTGGAGCGGAGCGTCCGTGAGCGCTTCCCTGCTGGCAGCTGATCTGAC 934

```

```

302 .....AlaProGluLeuLeuGlyProSer 310
935 CCCCTTATTATTATTCATCCCTTGGCACCACCTTGCACGTGAAGAGG 984
311 ValPheLeuPhe.....ProProLysPProLysAspThr..... 321
985 CTTTTTTTAAATAGAGAAATGAGTTTCT 1015
322 LeuMetIleSerArgThrProGluValThr 331

seq_name: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:US-08-243-010-1
seq_documentation_block:
; Sequence 1, Application US/08243010
; Patent No. 5639597
; GENERAL INFORMATION:
; APPLICANT: Lauffer, Leander
; APPLICANT: Zeitmeisel, Gerd
; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
; TITLE OF INVENTION: Production and Use Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,010
; FILING DATE: 13-MAY-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/798,564
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: DE P 40 37 837.3
; FILING DATE: 28-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32, 220
; REFERENCE/DOCKET NUMBER: 02481-1132-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 486 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-243-010-1

alignment_scores:
Quality: 347.50 Length: 231
Ratio: 2.613 Gaps: 7
Percent Similarity: 57.576 Percent Identity: 33.766

alignment_block:
US-09-006-352-1 x US-08-243-010-1
Align seg 1/1 to: US-08-243-010-1 from: 1 to: 486
10 GCTCAGCAGAGGAGGAGGCGCTGAGGAGGCGCGCTGCGGTGCT 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 AlarovalAlaValAlaAlaLeu..AlaValGlyLeuLeuLeuThr 17

```







```

439 ATTGCCCCGGGACCCCGACAGACAGCATGCGCACCCCTGGCCCCC 488
    ::::: ::::: ::::: ::::: ::::: :::::
152 AlaSerSerArgAlaProbsnGlyAsnValLeucylsValaCysAlaPr 168
    ::::: ::::: ::::: ::::: ::::: :::::
489 AGGCACTCTTCAGCCAGCATCTCCAGCAGAGCATGCGGCCCGCC 538
    ||||| ||||| ||||| ||||| ||||| |||||
168 oclyThrPheSerAspThrThrSerSerThrAspValCysArgProHisA 185
    ||||| ::::: ::::: ::::: ::::: ::::: :::::
539 GCAACTGCACGGCCCTGGGCGCTGAGCCCTCAATGTCAGAGCTTCCTCC 588
    ||||| ::::: ::::: ::::: ::::: ::::: :::::
185 rGileCysSerIleLeuAla.....IleProGlyAsnAlaSer 197
    ::::: ::::: ::::: ::::: ::::: :::::
589 CATGACACCCCTGTCCACAGCTGCACTGCGCTCCCGCTCAGCACCAGG 638
    ||||| ::::: ::::: ::::: ::::: ::::: :::::
198 ThrAspAlaValCys.....Al 203
    ::::: ::::: ::::: ::::: ::::: :::::
639 ACCAGAGCTGAGAGTGTGAGCGTCCGCTCATGCACTTTGTGCTTTC 688
    :||| ||| ::::: ::::: ::::: ::::: ::::: :::::
203 aPro.GluSerProThrLeuSerAlaIleProArgThrLeuTyValSer 219
    ::::: ::::: ::::: ::::: ::::: :::::
689 AGGACATCTCATCAAGAGCTGCAAGCGGCTGCTGAGGCCCTCGAGGCC 738
    ::::: ::::: ::::: ::::: ::::: :::::
220 GluProGluProThrArg.SerGluProLeuAspGlnGluPro...GlyP 235
    ::::: ::::: ::::: ::::: ::::: :::::
739 CCGGA.....GGGCTGCGCTCC..... 755
    ||::: ::::: ||||| |||||
235 roSerGluThrProSerIleLeuThrSerLeuGlySerThrProIleIle 251
    ::::: GACACCAAGGCGGG.....CCGCGGGCGCTTCAGACTGA 790
756 .....GACACCAAGGCGGG.....CCGCGGGCGCTTCAGACTGA 790
    ::::: ||||| ||||| ||||| ||||| :::::
252 GluGlnSerThrIleGlyIleSerLeuProIleGlyLeuIleValG1 268
    ::::: ||||| ||||| ||||| ||||| :::::
791 AGCTGCTGGGGCGGCTCAGAGCTCTGGGGCGCCAGAGCGGGCGCTG 840
    ::::: ||||| ||||| ||||| ||||| :::::
268 yValThrSerLeuGly.LeuLeuMetLeuGlyLeuValAsnCysIleIle 284
    ::::: ||||| ||||| ||||| ||||| :::::
841 CTGGTCGGGCTGCTGAGGCGCTGCGGCTGCGCCAGAGATGCCGGGCTGA 890
    ||||| ::::: ||||| ||||| ||||| :::::
285 LeuValGln.....ArgLysLysLysProSerCysLeuG1 296
    ::::: ::::: ::::: ::::: ::::: :::::
891 GCGAGAGCTCGCTGAGCGCTTCCTCCT 918
    ::::: ::::: ::::: ::::: ::::: :::::
296 naGAspAlaLysValProHisValPro 305

```







```

34  toThrTyrProTrrPaRgspAlaGluThrGlyGluArgLeuValCysAla 50
211 CCACCTACCCCTGGCGGAGCCAGAGAGAGGAGCGGCTGCTGGCGCC 260
51  GlnCysProproGlyThrPheValGlnArgProCysArgArgAspSerPr 67
261 CAGTGGCCCCCAGGACCTTTGTGACGGGGCGGTGGCCGAGACAGGCC 310
67  oThrThCysGlyProCysPropoArgHisTyrThrGlnPheTrrpant 84
311 CACACAGTGTGGCCGCTGTCCACCGGCGCCACATACGACGATGTGTGACT 360
84  yLeuGluArgCysArgTyrCysAsnValLeuGlyGluArgGlu 100
361 ACCTGGAGCGCTGCGCTACTGCAACGCTCTCGGGGAGCGGAGAG 410
101 GlnAlaArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgTh 117
411 GAGGACGGGCTGTCCACGACCCACACACCGTGCCTGCCCTGCCGAC 460
117 rGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysProp 134
461 CGCCTTCTTCGCGCAGCTGTCTGCTGTGAGCAGCAGCATGTGTCCAC 510
134 rGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCys 150
511 CTGGTGGCGGGGTATGCCCCGGGGCACCCCGACAGAACACGACAGTGC 560
151 GlnProCysPropoGlyThrPheSerAlaSerSerSerSerSerGluG 167
561 CAGCCGTGCCCCCGAGGACCTTCTCAGCCAGCAGCTCCACCTCAGAGCA 610
167 nCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValP 184
611 GTGCACAGCCCGACCACTCCACGCGCTGCGCTGCGCTCATATGTGC 660
184 rGlySerSerSerHisAspThrLeuGlySerSerSerSerSerGlyPhePro 200
661 CAGGCTCTCTCCCATGACACCTGTGACACAGCTGACAGCGCTTCCC 710
201 LeuSerThrArgValProGlyAlaGluGluCysGluArgAlaValIleAs 217
711 CTCAGCACCCAGGTAACAGAGAGTGTAGAGTGTGCGCTGCATCGCA 760
217 pPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArgLeuG 234
761 CTGTGTGCTTTCACGACATCTCCATCAAGAGCTGCAGCGCTGCTGC 810
234 IlnAlaLeuGluAlaProGluGlyTrrGlyProThrProArgAlaGlyArg 250
811 AGGCCCTCGAGAGCCCGGAGGGGTGGGCTCCGACACCAAGGGCGGCGC 860
251 AlaIleLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuGlyAl 267
861 GCGGCTTGGCAGCTGAAGCTGCTGGGGGCTCAGCGAGCTCTGGGGGC 910
267 aglAsnGlyAlaLeuLeuValArgLeuGlnAlaLeuAsnArgValAla 284
911 GCAGGACGGGGCGCTGCTGCTGGGCTCTCAGAGCGCTGCGCTGGCCA 960
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961 GGAATGCCGGGCTGTGAGGAGCGTCCGTGAGCGCTTCTCTCCGTGTGAC 1010

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seq\_name: /cgn2.6/prodata/2/lna/5A\_COMB.seq:us-08-974-022-5

seq\_documentation\_block:  
; Sequence 5, Application US/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.

```

? APPLICANT: Calzone, Frank J.
? APPLICANT: Chang, Ming-Shi
? TITLE OF INVENTION: OSTEOPROTEGERIN
? NUMBER OF SEQUENCES: 53
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Amgen Inc.
? STREET: 1840 Dehavenland Drive
? CITY: Thousand Oaks
? STATE: California
? COUNTRY: USA
? ZIP: 91320-1789
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/974,022
? FILING DATE: 12-DEC-1995
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/577,788
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Winter, Robert B.
? REFERENCE/DOCKET NUMBER: A-378
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1355 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 94..1296
? US-08-974-022-5

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  Ratio: 3.086                        Gaps: 5  
Percent Similarity: 64.732            Percent Identity: 38.839

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US-09-006-352-2 x US-08-974-022-5 ..

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67  AAGCCCTGAGGTTCCGGGAGCACCAATGACAGAGTGTGTGTGGCGC 116
15  lLeuAlaLeuProAlaLeuLeuProValProAlaValAlaGlyValAla 32
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117  GCTC.....GTCTTCTGGACATCTCCATTAAAGTGGACACCCAG 157
32  luptr.....ProThrTyrProTrrPaRgspAlaGluThrGlyGluArg 46
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
158  AAGGTTTCTCCAAAGTACCTTCATTATGACAGAAACCTCTCATCAG 207
47  LeuValAlaGlnCysPropoGlyThrPheValGlnArgProCysArg 63
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
208  CTGTTGTGTACAAATGCTCTCTGTGACTTAAACAAACACTGTATC 257
63  gArgAspSerProThrThCysGlyProCysPropoArgHisTyrThrG 80
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
258  AGCAAACTGGAAGACCGCTGTGCGCCCTTGCCTGACCACTACTACAG 307
80  lnpheTrrpAsnTyrLeuGluArgCysArgTyrCysAsnValLeuGly 96
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308  ACAGCTGACACACAGTGTGAGTGTATGTACAGAGCCCGCTGTGCAAG 357

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FEATURE:  
NAME/KEY: CDS  
LOCATION: 124..1326  
US-08-974-022-1

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Quality: 426.00 Length: 227  
Ratio: 2.979 Gaps: 4  
Percent Similarity: 62.996 Percent Identity: 38.326

alignment\_block:  
US-09-006-352-2 x US-08-974-022-1 ..

Align seg 1/1 to: US-08-974-022-1 from: 1 to: 2432

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20 AAlaLeuLeuProValProAlaValArgGly.ValAlaGlu..... 32
135 GCTGTGCTGTGCACTCTGCTGTCTTGTGACATTCATTGAATGGACACACC 184
33 .....ThrProThyTyProTTPatgAspAlaGluThrGlyGlu 45
185 AGGAACCTTTCCTCCAAATACTTGATTTATGACCCAGAAACCGACGCT 234
46 ArgLeuValCysAlaGlnCysProProGlyThrPheValGlnArgProCys 62
235 CAGCTCTGTGTGACAAATGTGCTCTGCGACACCTAACAAACAGCAGCTG 284
62 sArgArgAspSerProThrThrCysGlyProCysProProArgHisTyrT 79
285 CACACTGACGAGAGACACTGTGTGCTCCCTGCTGACTACTCTTATA 334
79 hGlnPheTyrPaspTyrLeuGluArgCysArgTyrCysAsnValLeuGly 95
335 CAGACAGCTGTGACACGATGATGATGATGATGATGATGATGATGATGAT 384
96 GAlGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAl 112
385 AAGGAACTGCACACCGCTGAACAGAGTGCACACCGCCACACACAGAGT 434
112 aCysArgCysArgThrGlyPhePheHisAlaGlyPheCysLeuGlu 129
435 GTGCGAATGTGAGAGAGGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 484
129 IsAlaSerCysProProGlyAlaGlyValIleAlaPheProGlyThrProSer 145
485 ACCGAGCTGTCCCGCCAGGCTTGGGTGCTGCGACGCGGAGACCCACAG 534
146 GlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSe 162
535 CGAAACACGCTTTCGAAAGATGTCCGATGCGCTCTGACAGGAGAGAC 584
162 rSerSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyL 179
585 GTCATCGAAGACACCCGTAGAGAACACACCACTGACGACGTCTTGGCC 634
179 euAlaLeuAsnValProGlySerSerSerHisAspThrLeuCysThrSer 195
635 TCCGCTCATTTTCAGAAAGCAATGCAACATGACATGCAATGTA..... 675
196 CysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu..... 210
676 TGTTCGGAACACAGAGACCACTAAATTTGTGATAGATGATGACCTT 725
211 CysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerTleL 227
726 GTGCGAAGAGCATTTCTGAGTTGTGCTGCTTACCAAGATTTATACCA 775
227 ysArgLeuGlnArgLeuLeuGlnAlaLeu 236
776 ATTGCTAGTGTCTGTGTCGACACATTTG 804
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seq\_name: /csgn2.6/prodata/2/lna/6A\_COMB.seq:US-08-974-022-3

seq\_documentation\_block:  
Sequence 3, Application US/08974022  
Patent No. 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 DenayVilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ. ID NO.: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1324 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: CDS  
LOCATION: 90..1292  
US-08-974-022-3

alignment\_scores:  
Quality: 424.50 Length: 205  
Ratio: 3.144 Gaps: 2  
Percent Similarity: 65.854 Percent Identity: 39.024

alignment\_block:  
US-09-006-352-2 x US-08-974-022-3 ..

Align seg 1/1 to: US-08-974-022-3 from: 1 to: 1324

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165 CCAAGTACTTGTGCTTGTGACCCAGAAACAGACTGTATACGACAGCTGCTG 214
50 aGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerP 67
215 CAATGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
67 roThrThrCysGlyProCysProProArgHisTyrThrGlnPheTyrPasn 83
265 AGACATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 314
84 TyrLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGlu 100
315 ACCAGTATGATGATGTGTATGATGATGATGATGATGATGATGATGATG 364
100 uGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgT 117
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[illegible]

seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-385-229-3

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seq.documentation_block:
Sequence 3, Application US/08385229
Patent No. 5605690
GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TNF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,229
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,236
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 3:

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? SEQUENCE CHARACTERISTICS:
? LENGTH: 1557 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? IMMEDIATE SOURCE:
? CLONE: INFR/FC Fusion Protein
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1557
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 1..1554
? OS-08-365-229-3

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alignment_scores:
  Quality: 355.50
  Ratio: 2.222
Percent Similarity: 56.537
Percent Identity: 32.155
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alignment\_block:  
US-09-006-352-2 x US-08-385-229-3

Align seg 1/1 to: US-08-385-229-3 from: 1 to: 1557

[illegible]



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638 TCTGTAACCTGCTGCGC.....ATCCCTGGGAATGCAAGCATG 675
190 AspThrLeuGlySerThrGlyPheProLeuSerThrArgValPr 206
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
676 GATGAGCTGCTGAGCTCCAGCTCC.....CCACCCGGATATAGGCC 719
206 GGLVALAGLUGLUCYSGIARGALAVALLLeaspheValAlaPheGln 223
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
720 AGGGGACATACCTTACCCCAAGCA.....GTGTCACACCAT 757
223 spIleSerIleLys ArgLeuGlnArg.....LeuLeuGlnAlaLeuG 237
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
758 CCACACACAGCAGCCAGCTCCAGAACCCAGCAGCTGCTCCAGACCTCC 807
237 uAlaProGluGlyTrpGlyProThrProArg...AlaGlyArgAlaAla 253
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
808 TTCCTGCTCCCAATGGGCCCCAGCCCTCCAGCTGAAGGAGCAGCTGGCA 857
253 euGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGln 268
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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seq_documentation_block:
; Sequence 1, Application US/08385229
; Patent No. 5605690
;
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Cindy A.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Method of Treating TNF-Dependent
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,229
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,236
; FILING DATE:

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Wright, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0606
; TELEFAX: (206) 587-0606
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1641 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Fibroblast

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; CELL LINE: WI-26 VAA
; IMMEDIATE SOURCE:
; LIBRARY: WI-26 VAA
; CLONE: Clone 1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..1473
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 154..1470
; FEATURE:
; NAME/KEY: s19-peptide
; LOCATION: 88..153
; US-08-385-229-1

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alignment_scores:
    Quality: 353.00      Length: 292
    Ratio: 2.234
    Percent Similarity: 54.110      Percent Identity: 31.507

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alignment\_block:  
US-09-006-352-2 x US-08-385-229-1 ..

Align seg 1/1 to: US-08-385-229-1 from: 1 to: 1641

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124 GAGCTGAGCTGCTGCGCTGCGGCGCAGCCTTCCGCC..... 162
24 lProAlaValAlaGlyValAlaGluThrProThrTrpProThrArgAsp 41
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163 .....CAGTGGCATTTTACACCTTACGGCCG..... 189
41 lAgThrGlyGlu..... 45
190 ..GAGCCGGGAGCATGCGCGCTCGAGATATCTGTACACAGACAGCT 237
46 ArgLeuValAlaGlyAlaGlnCysProProGlyThrPheValGlnArgProCys 62
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238 CAGATGCTGTCAGCAAAATGCTCGCCGGGCAACATGCAAGCTTTCTG 287
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388 AGCTTCGACCGAGTGAACATCAAGCTCGACATCGGGAACAGAACCGCAT 437
112 acGysArgCysArgThrGlyPhePheAlaHisAlaGly..... 124
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438 CTGACACTGACAGCGCGCTGTACTCGCGCTGAGACAGACAGAGGCT 487
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140 AlaProGlyThrProSerGlnAsnThrGlnCysGlnProCysProProG 156
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538 AGACGAGAACTGAACATCAGACAGCTGTGTGAGAGCCGTGCTCCCGGG 587
156 yThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArg 173
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588 GACGCTTCCCAACACGACTTCATCCACGATATTGTGACGCCACACAGA 637
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676 GATCAGCTGCTGACGTCCAGCTCC.....CCACCCGAGTATAGGCCCC 719
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720 AGGGGAGTACACTTACCCAGCCA.....GTGTCCACACGAT 757
223 spIleSerIleLys.ArgleuGlnArg.....leuGlnAlaIleuGl 237
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seq_documentation_block:
: Sequence 1, Application US/08650000
: Patent No. 5945397
: GENERAL INFORMATION:
: APPLICANT: Smith, Craig A.
: APPLICANT: Goodwin, Raymond G.
: APPLICANT: Beckmann, M. Patricia
: TITLE OF INVENTION: Tumor Necrosis Factor Receptors
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: U.S.A.
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/650,000
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/468,453
: FILING DATE:
: APPLICATION NUMBER: US/08/038,765
: FILING DATE:
: APPLICATION NUMBER: US 403,241
: FILING DATE: 05-SEP-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 405,370
: FILING DATE: 11-SEP-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 421,417
: FILING DATE: 13-OCT-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 523,635
: FILING DATE: 10-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Wight, Christopher L.
: REGISTRATION NUMBER: 31,680
: REFERENCE/DOCKET NUMBER: 2501-D
: TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Fibroblast
CELL LINE: WI-26 VAA
IMMEDIATE SOURCE:
LIBRARY: WI-26 VAA
CLONE: 1
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1473
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 154..1470
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 88..153
PUBLICATION INFORMATION:
AUTHORS: Smith, Craig A.
AUTHORS: Davis, Terri
AUTHORS: Anderson, Dirk
AUTHORS: Solam, Lisabeth
AUTHORS: Beckmann, M. P.
AUTHORS: Jerzy, Rita
AUTHORS: Dower, Steven K.
AUTHORS: Cosman, David
AUTHORS: Goodwin, Raymond G.
TITLE: A Receptor for Tumor Necrosis Factor Defines
TITLE: an Unusual Family of Cellular and Viral Proteins
JOURNAL: Science
VOLUME: 248
PAGES: 1019-1023
DATE: 25-MAY-1990
US-08-650-000-1

alignment_scores:
Quality: 353.00 Length: 292
Ratio: 2.234 Gaps: 11
Percent Similarity: 54.110 Percent Identity: 31.507

alignment_block:
US-09-006-352-2 x US-08-650-000-1 ..
Align seg 1/1 to: US-08-650-000-1 from: 1 to: 1641
8 GlyLeuSerLeuCysLeuValIleuAlaProAlaLeuProVa 24
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 GACTGAGCTCTGGGCTGGCGACGCTTGCCTGCCGCG..... 162
24 lProAlaValArgGlyValAlaGluThrProThrTyrrProTrpArgAspA 41
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
163 .....CAGGTGGCATTACACCTACGCCCG..... 189
41 lAgIuThrGlyGlu..... 45
190 ..GAGCCCGGAGCACATCGCGCTCAGAGAATACTATGACCAGACACT 237
46 ArgleuValYsAlaGlnCysProProGlyThrPheValGlnArgProcy 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
238 CAGATGTGCTGACGCAATGTCTCGCGCGGCCACATGCAAAAGCTCTTG 287
62 sArgArgAspSerProThrThrCysGlyProCysProProArgHisTyrr 79
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288 TACCAAGACCTGGACCGCTGTGACTCTCTGTAGACAGACATATCA 337
79 hrGlnPheTyrPasnTyrLeuGluArgCysArgTyrCysAsnValLeuCys 95
338 CCCAGCTCTGGAACTGGGTCCCGAGTGTGAGTGTGGCTCCCGCTGT 387
96 GlyAlaArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAl 112
388 AGCTGTGACAGGAGGAAATCAAGCCCTGACCTGGCAAGCAACCCGAT 437
112 aCysArgCysArgTyrGlnPhePheAlaHisAlaGly..... 124
438 CTGCACCTGCAGAGCCCGCTGTGACTGCGCGTGAAGCAAGAGAGGCT 487
125 ....PheCysLeuGluHisAlaSerCysProGlyAlaGlyValIle 139
488 GCGGCTGTGCGCGCGCTGCGCAAGTCCGCGCGCTTGGCGCTGGCC 537
140 AlaProGlyThrProSerGlnAsnThrGlnCysGlnProCysProProG 156
538 AGACGAGAACTGAACAATCAACACGTGTGTGACAGCCCTGTGGCCGG 587
156 yThrPheSerAlaSerSerSerSerSerSerGluGlnCysGlnProHisArg 173
588 GACGTTCTCCAAACGACTTCATCCACGAAATTTGCAAGGCCCAACGCA 637
173 snCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 189
638 TCTGTAACTGTGTGCC.....ATCCCTGGGAATGCAAGCATG 675
190 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValPr 206
676 GATGAGCTGACAGTCCACCTGCC.....CCCAACCCGAGTATGGCCCC 719
206 GGLYAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGln 223
720 AGGGGCACTACACTTACCCAGCCA.....GTGTCCACACGAT 757
223 spIleSerIleLys ArgLeuGlnArg.....LeuLeuGlnAlaLeuG 237
758 CCCAAGACAGCAGCACTCCAGAACCCAGACAGCTCCCAAGACCTCC 807
237 uAlaProGluGlyTyrGlyProThrProArgAlaGlyArgAlaAlaLeu 254
808 TTCTGCTCCCAATGGCCCAAGCCCC.....C 836
254 InLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAspG 270
837 AGCTGAAG.....GGA 847
271 AlaLeuLeuValArgLeuLeuGln 278
848 GCACCTGGGAGCTTGCCTCTCCAG 871
seq_name: /cgn2_6/prodata/2/lna/backfiles1.seq:5395760-1
seq_documentation_block:
; Patent NO. 5395760
; APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,
; M. PATRICIA
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-2 AND
; B-RECEPTORS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/523,635
; FILING DATE: 10-MAY-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION NUMBER: 405,370
; FILING DATE: 11-SEP-1989
; APPLICATION NUMBER: 403,241

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; FILING DATE: 05-SEP-1989
; SEQ ID NO: 1
; LENGTH: 1641
5395760-1

Alignment_scores:
  Quality: 353.00      Length: 292
  Ratio: 2.234        Gaps: 11
  Percent Similarity: 54.110      Percent Identity: 31.507

alignment_block:
US-09-006-352-2 x 5395760-1

Align seg 1/1 to: 5395760-1 from: 1 to: 1641

8 GlyLeuSerLeuLeuCysLeuValLeuAlaLeuProAlaLeuLeuProVa 24
1124 GGAAGTGAAGCTGTGGCTGGCGGCGACGCGCTTGCAGCC..... 162
24 1ProAlaValArgGlyValAlaGluThrProThrTyrProThrArgAsp 41
163 .....CAGGTGGCAATTACACCCCTAGCCCG..... 189
41 LagluThrGlyGlu..... 45
190 ..GAGCCCGGAGCAGATGCCGCTCAGAGAAATATGATGACAGAGAGCT 237
46 ArgLeuValCysAlaGlnCysProProGlyThrPheValGlnArgProCy 62
238 CAGATGTGCTGCAGCAAAATGCTCCGCGCCCAACATGCAAAAGTCTTG 287
62 sArgArgAspSerProThrThrCysGlyProCysProProArgHisTyrT 79
288 TACCAAGACCTCGGACACCGCTGTGTGACTCTGTGAGAGACAGACATAA 337
79 hrGlnPheTyrPasnTyrLeuGluArgCysArgTyrCysAsnValLeuCys 95
338 CCCAGCTCTGGAACTGGGTCCCGAGTGTGAGTGTGGCTCCCGCTGT 387
96 GlyAlaArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAl 112
388 AGCTGTGACAGGAGGAAATCAAGCCCTGACCTGGCAAGCAACCCGAT 437
112 aCysArgCysArgTyrGlnPhePheAlaHisAlaGly..... 124
438 CTGCACCTGCAGAGCCCGCTGTGACTGCGCGTGAAGCAAGAGAGGCT 487
125 ....PheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIle 139
488 GCGGCTGTGCGCGCGCTGCGCAAGTCCGCGCGCTTGGCGCTGGCC 537
538 AlaProGlyThrProSerGlnAsnThrGlnCysGlnProCysProProG 156
156 yThrPheSerAlaSerSerSerSerSerSerGluGlnCysGlnProHisArg 173
588 GACGTTCTCCAAACGACTTCATCCACGAAATTTGCAAGGCCCAACGCA 637
173 snCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 189
638 TCTGTAACTGTGTGCC.....ATCCCTGGGAATGCAAGCATG 675
190 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValPr 206
676 GATGAGCTGACAGTCCACCTGCC.....CCCAACCCGAGTATGGCCCC 719
206 GGLYAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGln 223
720 AGGGGCACTACACTTACCCAGCCA.....GTGTCCACACGAT 757
223 spIleSerIleLys ArgLeuGlnArg.....LeuLeuGlnAlaLeuG 270

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; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
; B-RECEPTORS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/523,635
; FILING DATE: 10-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION NUMBER: 405,370
; FILING DATE: 11-SEP-1989
; APPLICATION NUMBER: 403,241
; FILING DATE: 05-SEP-1989
; SEQ ID NO:3
; LENGTH: 3813
5395760-3

alignment_scores:
  Quality: 332.50      Length: 273
  Ratio: 2.173        Gaps: 9
  Percent Similarity: 56.044  Percent Identity: 29.670

alignment_block:
-us-09-006-352-2 x 5395760-3 ..

Align seg 1/1 to: 5395760-3 from: 1 to: 3813

46 ArgLeuValCysAlaGlnCysProProGlyThrPheValGlnArgProCys 62
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208 CAGATGCTGCTGTAATGTCCTCGCCCAATATGTGAACAATCTTGCG 257
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
62 SARGrArGspSerProThrPheCysGlyProCysProProArgHisTyrT 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
258 CAACAAGACCTCGGACACCTGTGTGCGGACTGAGCGCAAGCATGTATA 307
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
79 hrgInPheTrpAspTyrLeuGluArgCysArgTyrCysAsnValLeuGly 95
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
308 CCCAGGTGTGAGACCATGTTGCTGATCTTTGAGAGTGCAGTCTTCCCT 357
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
96 GlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAl 112
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
358 ACCACTGCACAGGTGAGATGCGCGCTGCACTAAACAGCAAGACCGAGT 407
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
112 ACysArgCysArgThrGlyPhePhe.....AlaHisAlaGlyP 125
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408 GTGTGCTTGGCAAGCTGCGAGCTACTGCGCCTTGAAACCCATCTTGCA 457
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125 he.....CysLeuGluHisAlaSerCysProProGlyAlaGlyVal 138
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139 lLeAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCysProPr 155
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508 GCCAGTTCAGAGCCCAATGAAATGTGCTATGCAAGCGCTGAGCCG 557
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155 OGlyThrPheSerAlaSerSerSerSerGlnGlnCysGlnProHisA 172
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558 AGGCGAGCTTCTGTGACACCATCATCTGATGTGTGAGGCCGCCGCC 607
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172 rGAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSer 188
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608 GCATCTGTACATCTGCTGCT.....ATTCGCCGAATGCAAGC 645
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189 HisAspThrLeuGlyThr.....SerCysThrGlyPheProLe 201
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646 ACAGTGTGAGTCTGTGCGCCGAGCGCCCAACTCTAAATGCCATGCCAG 695
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201 uSerThrArgValProGlyAlaGluGluCysGluArgAlaVallLeasp 218
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656 GACACTTACGTATCTAGCCAGAGACCCACACAGCCCAACCCCTGGAT 744
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
218 heValAlaPheGlnAspIleSerIleTyrArgLeuGlnArgLeuLeuGln 234
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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235 AlaleuGluAlaProGluGlyTyrPglYProThrPro..... 246
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784 TCCTTG.....GGTCAACCCCACTATTTGAAACAAG 815
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247 ArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrG 263
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816 TACCAAGGTGCGCATCTCTCTCCCAATTTGGCTGTGAGTGCAT 865
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866 CACTG.....GGTCTGCTGATGTAGAGCTGTGAACTGC 900
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280 Leu.....ArgValAlaArgMetProGlyLeuGluArgSerVa 292
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901 ATCATCTCTGTGACAGAGAAAGAACCCCTCTGCTTACAAAGATGCG 950
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seq_name: /cgn2_6/plodata/2/lna/5A.COMB.seq:us-08-266-080B-12

seq_documentation_block:
; Sequence 12, Application US/08266080B
; Patent No. 5606031
; GENERAL INFORMATION:
; APPLICANT: Jack Lile
; APPLICANT: Tadahiko Kohno
; APPLICANT: Duane Bonam
; APPLICANT: Mary S. Rosendahl
; TITLE OF INVENTION: Production of Biologically Active
; TITLE OF INVENTION: Recombinant Neurotrophic Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,080B
; FILING DATE: 27-JUNE-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,122
; FILING DATE: 09-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/087,912
; FILING DATE: 06-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/680,681
; FILING DATE: 04-APRIL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/594,126
; FILING DATE: 09-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/547,750
; FILING DATE: 02-JULY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/505,441
; FILING DATE: 06-APRIL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: SYNE200C5
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 691 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-266-080B-12

alignment_scores:
Quality: 324.00      Length: 184
Ratio: 2.945         Gaps: 4
Percent Similarity: 59.783   Percent Identity: 34.239

alignment_block:
US-09-006-352-2 x US-08-266-080B-12 ..

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46 .....ArgLeuValCysAlaG 51
189 CTGCCGGCTAGAGAACTATGATACCGACAGAGCTCAGATGCTGCAGCA 238
51 LncGlyProGlyThrPheValGlnArgProCysArgArgAspSerPro 67
239 AGTGCCTCGCGGCGACATGCAAAAGCTTCTGTACCAAGACTCGGAC 288
68 ThrThiCysGlyProCysProProGlnHisTyThrGlnPheTrpAsnTy 84
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
289 ACCGTGTGACTCTCTGTAGAGACAGCACAATACACCGAGCTGTGAACTG 338
84 rLeuGlnArgCysArgTyrcysAsnValLeuCysGlyGlnArgGluGlu 101
339 GGTTCGCGAGTGGCTGTGAGCTGTGGCTCCGCTGAGCTGTGACAGGTGG 388
101 LuAlaArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThr 117
389 AAACCTCAAGCTGCACCTCGGGAACAGAACGCAATCTGACCTGCAGGCC 438
118 GlyPhehehAlaHisAlaGly.....PheCysLeuGlu 128
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439 GCGTGTGACTGCGCGCTGAGCAAGCAGAGCGGCTGCGCTGCGCGCC 488
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639 C.....ATCCCTGGAGATGCAGCAGGATGCAGTGTGCACGT 676
195 er 195
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677 CC 678

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seq_documentation_block:
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Sequence 12, Application PC/TUS9505423
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tadahlko Kohno
APPLICANT: Duane Bonam
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05423
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,090
FILING DATE: 27-JUNE-1994
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05423-12

alignment_scores:
Quality: 324.00      Length: 184
Ratio: 2.945         Gaps: 4
Percent Similarity: 59.783   Percent Identity: 34.239

alignment_block:
US-09-006-352-2 x PCT-US95-05423-12 ..

Align seg 1/1 to: PCT-US95-05423-12 from: 1 to: 691

30 ValAlaGluThrProThrTyProTPrArgAspAlaGluThrGlyGlu.. 45
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151 GTGCATTACACCTACGCTCG.....GAACGGGTTCTAC 188
46 .....ArgLeuValCysAlaG 51
189 CTGCCGGCTCAGAGAACTATGACACAGACAGTCAATGCTCAGCA 238
51 lncysproproglythrphenvalinarprocyargargaspserpro 67
239 AGCTCTCGCCGGCCACATGCAAAAGTCTTCTGTACCAAGACCTCGGAC 288
68 ThrThrCysGlyProCysProProArgHisTyrThrGlnPheTyrAspTyr 84
289 ACCGTGTGACTCCTGTGAGACACACATACACCCAGCTGTGAACTG 338
84 rleugluargcysargtyrcysasnvalleucysgyluarargluglug 101
339 GGTTCGCCAGTCTTGAAGCTGTGCTGCCGCTGTGACCTGTGACCAAGTGG 388
101 luAlaArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThr 117
389 AAACTCAGCCCTGCACCTCGGGAACGCAACCGCATCTGCACCTGCAGGCC 438
118 GlyPhePheAlaHisAlaGly.....PheCysLeuGlu 128
439 GGCTGTGACTCGCGCTGAGCAAGCAGGAGGGTCCGCTGTGCGGCC 488
128 uHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProS 145
489 GCTGCCGAAGTCCCGCCGGCTTGGCGGCCAGACCTGAACTGAA 538
145 erGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSer 161
539 CATCAGAGCTGTGTGCAAGCCCTGTGCGCCGGGACCTTCTCCACACAG 588
162 SerSerSerSerGlnGlnCysGlnProHisArgAsnCysThrAlaLeuGlu 178
589 ACTTCATCCACGGATTTTGCAGGCCCAACGATCTGTACGTGTGTC 638
178 yLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCysThrS 195
639 C.....ATCCCTGGAAATGCAAGCAGGATGACAGTGCACAGT 676
195 er 195
677 CC 678

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GenCore version 4.5  
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OM protein - protein search, using SW model

Run on: October 31, 2001, 12:36:51 ; Search time 17.3 Seconds

(without alignments)  
1320.946 Million cell updates/sec

Title: US-09-006-352-2

Perfect score: 1634

Sequence: 1 MRALEGPGLSLCLVLALPA.....RVARRPGLERSRERFLPVA 300

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	351.5	20.5	461	1 A35356	tumor necrosis fac
2	333.5	20.4	459	2 I48854	gene murine tumour
3	332.5	20.3	474	2 B38634	tumor necrosis fac
4	315	19.3	435	2 I54182	tumor necrosis fac
5	262.5	16.1	349	2 D72175	g2r protein - vari
6	262.5	16.1	349	2 D36858	gene G4R protein -
7	262	16.0	348	2 T26623	hypothetical prote
8	236.5	14.5	325	2 B43692	T2 protein - rabbl
9	226	13.8	277	2 I37552	OX40 homolog - hum
10	215	13.2	326	1 GQVZML	T2 protein - myxom
11	214	13.1	271	2 S12783	OX40 antigen precu
12	211	12.9	277	2 A60771	B-cell activation
13	203	12.4	305	2 A46476	B cell-associated
14	198.5	12.1	272	2 I48700	gene ox40 protein
15	186.5	11.4	595	2 A42086	CD30 antigen precu
16	185	11.3	256	2 B32393	T-cell antigen 4-1
17	176	10.8	416	1 JN0006	neuro growth facto
18	175.5	10.7	427	1 GQHNUN	neuro growth facto
19	174	10.6	255	2 I38426	lymphocyte activat
20	170	10.4	425	1 A26431	nerve growth facto
21	159.5	9.8	260	1 A46517	CD27 antigen precu
22	155.5	9.5	327	2 A46484	apoptosis-mediatin
23	148.5	9.1	1574	2 T13954	MEG6 protein - ra
24	148	9.1	250	1 A49053	CD27 antigen precu
25	147.5	9.0	5376	2 T42215	zonadhesin - mouse
26	145	8.9	335	2 A40036	apoptosis-mediatin
27	144	8.8	324	2 JC2395	Fas antigen precu
28	143.5	8.8	1289	2 T43251	furin (PC 3.4.21.7
29	143	8.8	1620	2 T27283	hypothetical prote

#### ALIGNMENTS

```

30. 140      8.6      314 2 I37383      FAS soluble protei
31. 137.5    8.4      454 1 GOMST1      tumor necrosis fac
32. 135      8.3     2321 1 S78549      notch3 protein - h
33. 133      8.1     493 2 JCS486      membrane glycoprot
34. 129.5    7.9     1548 2 S34583      serine proteinase
35. 128.5    7.9     3635 2 T10053      laminin alpha 5 ch
36. 127      7.8     1192 2 S69000      laminin gamma 2 ch
37. 125.5    7.7     461 1 GQRTT1      tumor necrosis fac
38. 125.5    7.6     1255 1 A24571      adhesive ligand ep
39. 124.5    7.6     1713 2 A55347      laminin alpha-2 ch
40. 124.5    7.6     3106 1 S53868      tumor necrosis fac
41. 123.5    7.6     455 1 GQHTT1      hypothetical prote
42. 122.5    7.5     2824 2 T22759      laminin gamma-1 ch
43. 120      7.3     1609 1 MSHUB2      notch 3 protein -
44. 120      7.3     2318 2 S45306      tumor necrosis fac
45. 119.5    7.3     461 2 JCA302

```

#### RESULT 1

```

A35356      tumor necrosis factor receptor 2 precursor [validated] - human
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text.change 08-Dec-2000
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower,
Science 248, 1019-1023, 1990
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a
A:Reference number: A35356; MUID:90260639
A:Accession: A35356
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SMI>
A:Cross-references: GB:M32315; NID:q189185; PIDN:AAA59929.1; PID:q189186
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
A:Reference number: A36475; MUID:91045991
A:Accession: A36475
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195, 'R', 197-461 <KOH>
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,
Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellul
A:Accession: A48416; MUID:91370690
A:Accession: A48416
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-461 <DEM>
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAI19824.1; PID:g235649
A:Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)
R:Hehlhar, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons
A:Reference number: A36007; MUID:90349572
A:Accession: A36007
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA61262.1; PID:g339752
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus,
J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor
A:Reference number: A23666; MUID:91060408
A:Accession: A23666
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOB>

```



R:Engelmann, H.; Novack, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
 A:Reference number: A35010; MUID:90110215  
 A:Accession: B35010  
 A>Status: Preliminary  
 A:Molecule type: Protein  
 A:Residues: 27-31 <ENG>  
 R:Kühnert, P.; Kemper, O.; Wallach, D.  
 Gene 150, 381-386, 1994  
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of  
 A:Reference number: I38094; MUID:9511934  
 A:Accession: I38094  
 A>Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-37 <RES>  
 A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701  
 C:Genetics:  
 A:Gene: GDB:TNFR2  
 A:Cross-references: GDB:I25914; OMIM:191191  
 A:Map position: 1p36.2-1p36.2  
 A:Note: the list of introns is incomplete  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
 F:40-76/Domain: NGF receptor repeat homology <NG1>  
 F:78-119/Domain: NGF receptor repeat homology <NG2>  
 F:120-162/Domain: NGF receptor repeat homology <NG3>  
 F:164-201/Domain: NGF receptor repeat homology <NG4>  
 F:262-279/Domain: transmembrane #status predicted <TMN>  
 F:280-461/Domain: intracellular #status predicted <INT>  
 F:11.193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.5%; Score 351.5; DB 1; Length 461;  
 Best local Similarity 29.8%; Pred. No. 4,5e-19;  
 Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;  
 QY 8 GLSLCLVLAIPALPPAVAGVETPTTWRDAETGE-----RLVCAQCPG 55  
 DB 13 GLELMAAHALPA-----QVAFETYPAR-----EPSTRLRLRYDQTAOMCCSKCPG 60  
 QY 56 TVQVQPCRRDSPPTGCPPRHYTOFWNYLERCRVCNVLCGEREEARACHATINRACRC 115  
 DB 61 QHAVFCTKTSIDTVCDSCEDSTYTQILNMWPECLSCGSKSDQVETQACTREONRICTC 120  
 QY 116 RTGFEAHAG-----FLEHASCPGAGVIAPTGPTSONTOCOPCPGTFSSASSSBOCQ 169  
 DB 121 RPYGVYCALSKQEGRLCAPRKCPGFGVAPPTETSDVYCKCAPCTFSNTSTSDICR 180  
 QY 170 PHRNCTALGLALNVPGSSSHDTLCTGTFPLSTRVPGAECEERAVDFVAFODISIKRL 229  
 DB 181 PHQICNVVA-----IPGNASMDAVCTSTS--PTRSMAFGAHLHPQV-----STRSQHT 227  
 QY 230 QRLQALEAPE-----GWCPTPRA-----GRAALQKRLRLTELGLAQDQALVRLLOAL 280  
 DB 228 QPMPEPSTASTSTFLPMGSPSPAGESTGDFALPVGLIVGTAL-----GLLITGVNVCV 282  
 QY 281 ---RVAMP--GLERSYVERFLP 298  
 DB 283 IMTVKKKKPCLCTGRKAKVPHLP 304

RESULT 2  
 148854  
 gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
 C:Accession: I48854  
 R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
 Mamm. Genome 5, 726-727, 1994

A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
 A:Reference number: I48854; MUID:95178848  
 A:Accession: I48854  
 A>Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-459 <RES>  
 A:Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 F:151-189/Domain: NGF receptor repeat homology <NGF>

Query Match 20.4%; Score 333.5; DB 2; Length 459;  
 Best local Similarity 29.7%; Pred. No. 1e-17;  
 Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;  
 QY 46 RLVCACCPGTFVQPCRRDSPPTGCPPRHYTOFWNYLERCRVCNVLCGEREEARAC 105  
 DB 37 OMCCACCPGQVYKHKCNKTSIDTVACADEASMYTQVWNOFRTLCSSSCSTQVETRAC 96  
 QY 106 HATHNRCRCRKTGFE-----AHAGF-----CLEHASCPGAGVIAPTGPTSONTOCOPCPGTF 158  
 DB 97 TKQNRVACACEAGRYCALKTHSGCRQCRKLSKCGFGVASSRANPANGVLCACAPGTF 156  
 QY 159 SASSSSBOCOPPHNCTALGLALNVPGSSSHDTLCT-----SCTGPFPLSTRVPGAECEERA 214  
 DB 157 SDTTSSTVDCRPHRICSTILA-----IPGNASTAVCAPESPILSAIPRLTYVSGPPTPSQ 212  
 QY 215 VIDFVAFODISIKRLQRLQALEAPEGWPPTP-----RGRRAALQKRLRLTELGLAQD 269  
 DB 213 PLD-----QERCGSQNPISLITSL-----GSTPIIDSTKGGISLIGLIVGTSL----- 257  
 QY 270 GALLVRLLOAL-----RVAMPGLERSYVERFLP 298  
 DB 258 GLMLGLVNCFLIVQKKRPSCLQKDAKVPYVP 290

RESULT 3  
 B38634  
 tumor necrosis factor receptor type 2 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
 C:Accession: B38634; A40254; S54816  
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto  
 A:Reference number: A38634; MUID:91187885  
 A:Accession: B38634  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <LEN>  
 A:Cross-references: GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:9199828  
 R:Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f  
 A:Reference number: A40254; MUID:91246168  
 A:Accession: A40254  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <GEO>  
 A:Cross-references: GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:9199828  
 R:Kismonopis, M.; Fellous, R.; Feldmann, M.; Chennajovsky, Y.  
 submitted to the EMBL Data Library May 1995  
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor  
 A:Reference number: S54816  
 A:Accession: S54816  
 A>Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-22 <NIS>  
 A:Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA50618.1; PID:9809044  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: cytokine receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
 F:40-77/Domain: NGF receptor repeat homology <NG1>  
 F:79-120/Domain: NGF receptor repeat homology <NG2>



F:166-203/Domain: NGF receptor repeat homology <MG4>

Query Match 20.3%; Score 332.5; DB 2; Length 474;

Best Local Similarity 29.7%; Pred. No. 1.2e-17;

Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

OY 46 RLVCACCPGPTVQRCRDRSDPTTCGPPRRHYTQFWNLERCRCNVLCGEREEBARAC 105  
::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||  
DB 52 QMCAACPCPGYVKHPCNKTSPTVCADCEASMTYQWNGFRITLSCSSSCCTTQVEIRAC 111  
OY 106 HATHNACRCRGFF-----AHAGF---CLEHASCPPGAGVIAPGTSONTOCPCEPTGF 158  
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||  
DB 112 TQOONVVCACEAGRYCALKTHSGSCQCKMRLSKCGPGFVASSRAPNGVNLCAKACAPGT 171  
OY 159 SASSSSECCOPHRNCTAGLNLVPGSSSHDTCT-----SCGFPPLSTRVPGAECCERA 214  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 172 SDTSTSDVCRPRICSIILA-----IPGNASTDVACAPESPTLSAIRPTLYVSOPEPTRSO 227  
OY 215 VIDPVAQDLSIKRLQRLQALEAPEGWGPPT-----RAGRAALQLKRRRLTELLGAOD 269  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 228 PLD---GEGPSGQTPSILITSL-----GSTPIEGSTKGISLPIGLIVGTSI----- 272  
OY 270 GALVLRLOAL-----RVANMPGLERSVRRERFLP 298  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 273 GLMLGLVNCILVORKKKRPSCLORDAKVPHVP 305

#### RESULT 4

tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000

C:Accession: I54182

R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Bergh, H.; Marynen, P.

Genomics 16, 214-218, 1993

A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen

A:Reference number: I54182; MUID:93252381

A:Accession: I54182

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-435 <RES>

A:Cross-references: GB:I04270; MID:9339761; PIDN:AAA36757.1; PID:9339762

C:Genetics:

A:Gene: GDB:LTBR

A:Cross-references: GDB:1230195; OMIM:600979

A:Map position: 12p13.3-12p13.1

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 19.3%; Score 315; DB 2; Length 435;

Best Local Similarity 31.8%; Pred. No. 2.3e-16;

Matches 89; Conservative 29; Mismatches 120; Indels 42; Gaps 12;

OY 3 ALEGPGLSLCLVLAIPALLPVAVGVAETPTV-----PWRDA-----ETGERLVCAQC 52  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 6 ATAPGGLAMPVLVLGFLGLAASQPAV---PPYASENQCRCRQEKYEPQHRICCSRC 62  
OY 53 PRCPTFYQRCRDRSDPTTCGPPRRHYTQFWNL---ERCRCNVLCGEREEBARACHATH 109  
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||  
DB 63 PRCTVYSACRSIRIDYVCAICATCAENSYNEHNNYITCOLCRPCDPVWG--LEETAPCVSKR 120  
OY 110 NRACRCRTGFEFAHAGFCL--H---ASCPGCA-GVIAPGTSPQONQOCPCPGTGSASS 162  
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||  
DB 121 KTCRCRQPGKFC-AAVALECTHCELLSDCPGGEALIKDEVGNGNHCVPCKRGHONT 179  
OY 163 SSSSECCOPHRNCTAGLNLVPGSSSHDTCTGTFPLSTRVPGAECCERAVIDPVAQ 222  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 180 SPARQCPHRCRNOGIVLEAPGTAOSDTTCCKNPLE-PLPEKMSGTMLMLAVLLPLAFL 238  
OY 223 DIS-----IKRLQRLQALEAPEGWGPPTPRAG 249  
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 239 LLATVESCIMKSHPSLCRLKGLSLK--RRPQGGPNPVAG 276

#### RESULT 5

G2R protein - variola minor virus (strain Garcia-1966)

D72175

C:Species: variola minor virus

C>Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 20-Jun-2000

C:Accession: D72175

R:Shchelkunov, S.N.; Tolmanin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lo

submitted to GenBank, March 1998

A:Description: Analysis of the complete coding sequence of DNA of alastrim variola mi

A:Reference number: A72150

A:Accession: D72175

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <SHC>

A:Cross-references: GB:I16780; MID:9583055; PIDN:CA054798.1; PID:95830759

A:Experimental source: strain Garcia-1966

C:Genetics:

A:Gene: G2R

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 16.1%; Score 262.5; DB 2; Length 349;

Best Local Similarity 30.0%; Pred. No. 1.6e-12;

Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;

OY 9 LSLCLVLAIPALLPVAVGVAETPTVPRDAETGERLVCACCPGTFVQRCRDRSDPT 68  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 10 LFLSCITINGRDAAPPTPPNGKCKDTEY-----KRHNLCCLSCPPGTIASRLCDSKTNT 63  
OY 69 TCGPCPPRRHYTQFWNLERCRCNVLCGEREEBARACHATHNRCRRTGFF-----AH 122  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 64 QCRPGSGGTFITSNHNLPAALSCNGRCNSNQVETRSTNTHNHCESPCYCYLLKSSG 123  
OY 123 AGCLCHASCPCPGAGYIAPGTPSONTQOCPCPGTSSASSSSBQCPHNNCTALGALN 182  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 124 CKACVSOATKCGICIGYV-SGHTSVGDVLCSPCGGCTVSYVSSDCKEPPVNNFTFYDVE 182  
OY 183 VPSSSHDTLCTCTGFPPLSTRVPAE 209  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 183 ITLYPVNDTSCRTTGTGLESILTSE 209

#### RESULT 6

D36858

gene: G2R protein - variola virus

N:Alternate names: B28R protein (COP)

C:Species: variola virus

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Mar-2001

C:Accession: D36858; S46888; S32385; S35987

R:Blinov, V.M.

submitted to GenBank, November 1992

A:Reference number: A36859

A:Accession: D36858

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <BLI>

A:Cross-references: GB:X69198; MID:9456758; PIDN:CA049137.1; PID:9457087

A:Experimental source: strain India-1967, ssp. major, isolate Ind3

R:Kol'khalov, A.A.; Blinov, V.M.; Gylorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F

submitted to the EMBL Data Library, April 1992

A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H

A:Reference number: S46868

A:Accession: S46888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <KOL>

A:Cross-references: EMBL:X67117; MID:9516428; PIDN:CA047540.1; PID:9516449

A:Experimental source: strain India-1967, isolate Ind3

R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhtchev, U.S.

FEBS Lett. 319, 80-83, 1993

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protect



A:Reference number: S32385; MUID:93202281  
 A:Accession: S32385  
 A:Molecule type: DNA  
 A:Residues: 31-168 <SHC>  
 A:Cross-references: EMBL:X69198  
 A:Experimental source: strain Indla-1967, ssp. major  
 C:Gene: G4R  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
 F:37-66/Domain: NGF receptor repeat homology <NGF>  
 F:68-109/Domain: NGF receptor repeat homology <NG2>  
 F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 16.1%; Score 262.5; DB 2; Length 349;  
 Best Local Similarity 30.0%; Pred. No. 1.6e-12;  
 Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;  
 Oy 9 LSLICLVIALPALLPVAVGVAEPTPYPMRDAETGERLVCAOCPGPTFVORPCRRDSPT 68  
 Db 10 LFLSCIIINGDAAPYPPNCKKDEY-----KRHNLCCLSCPPGTVASRLDCKSTNT 63  
 Oy 69 TCGPCPRHYTOFWNYLERCYCNVLCGEREEBARACHATNRCRRTGFE-----AH 122  
 Db 64 QCPFGSGGTSTRNHNPACISGRCNSNOVETRSCNTTHNRICEGSPGYCILKSSG 123  
 Oy 123 AGFLEHASCPPGAGVAPGTPSONTOCOPCPGTFSSASSSSFCQPHRNCALGLALN 182  
 Db 124 CKACVSQTKGIGYGV--SGHTSVGDVICSFGFGTYSHTVSSADKCPVNNTFNYIDVE 182  
 Oy 183 VPGSSHDTICTSCGTGFPPLSTRVPGAE 209  
 Db 183 ITLYPVNDTSCRTTGTGLSESLTSE 209

RESULT 7  
 T28623  
 hypothetical protein G2R - variola major virus  
 C:Species: variola major virus  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
 C:Accession: T28623  
 R:Massung, K. F.; Esposito, J. J.; Liu, L. I.; Qi, J.; Utterback, T. R.; Knight, J. C.; Aubin  
 A:Title: Potential virulence determinants in terminal regions of variola smallpox virus  
 A:Reference number: Z20488; MUID:94088747  
 A:Accession: T28623  
 A:Status: preliminary; translated from GB/EMBL/DDHJ  
 A:Molecule type: DNA  
 A:Residues: 1-348 <MMS>  
 A:Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60933.1; PID:9439102  
 A:Experimental source: strain Bangladesh 1975  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 16.0%; Score 262; DB 2; Length 348;  
 Best Local Similarity 30.8%; Pred. No. 1.7e-12;  
 Matches 64; Conservative 28; Mismatches 100; Indels 16; Gaps 4;  
 Oy 9 LSLICLVIALPALLPVAVGVAEPTPYPMRDAETGERLVCAOCPGPTFVORPCRRDSP 67  
 Db 10 LFLSCIIINGDAAPYTP-----PMGKCKDEYKRHNLCCLSCPPGTVASRLDCKSTN 61  
 Oy 68 TTGPGCPRRHYTOFWNYLERCYCNVLCGEREEBARACHATNRCRRTGFE-----A 121  
 Db 62 TQCTPGSCFTSRNNHNPACISGRCNSNOVETRSCNTTHNRICEGSPGYCILKSSG 121  
 Oy 122 HAQFLEHASCPPGAGVAPGTPSONTOCOPCPGPTFSSASSSSFCQPHRNCALGLAL 181  
 Db 122 GCACACVSQTKGIGYGV--SGHTSVGDVICSFGFGTYSHTVSSADKCPVNNTFNYIDV 180  
 Oy 182 NVPGSSHDTICTSCGTGFPPLSTRVPGAE 209  
 Db 181 EITLYPVNDTSCRTTGTGLSESLTSE 208

RESULT 8  
 B43692  
 T2 protein - rabbit fibroma virus  
 C:Species: rabbit fibroma virus  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: B43692  
 R:Upton, C.; Delange, A. M.; McFadden, G.  
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer  
 A:Reference number: A43692; MUID:87321103  
 A:Accession: B43692  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-325 <UPT>  
 A:Cross-references: GB:M17433  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
 F:64-105/Domain: NGF receptor repeat homology <NG2>  
 F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 14.5%; Score 236.5; DB 2; Length 325;  
 Best Local Similarity 29.9%; Pred. No. 1.3e-10;  
 Matches 58; Conservative 25; Mismatches 94; Indels 17; Gaps 4;  
 Oy 11 LSLICLVIALPALLPVAVGVAEPTPYPMRDAETGERLVCAOCPGPTFVORPCRRDSPT 70  
 Db 8 LVCVVVYGDVYSSNCKGSHDY-----EKDGLCASCHPFGFVSRLOGPSNTVC 61  
 Oy 71 GCPRRHYTOFWNYLERCYCNVLCGEREEBARACHATNRCRRTGFE-----HAG 124  
 Db 62 SPEDGTFTASNNHNPACISGRCNSNOVETRSCNTTHNRICEGSPGYCILKSSG 121  
 Oy 125 FCLFHASCPPGAGVAPGTPSONTOCOPCPGTFSSASSSSFCQPHRNCALGLALNP 184  
 Db 122 ICAPQTKCPAGIGV--SGHTRAGDTLCKCPHPTSDLSPTERTSTFNTVSGRNL--- 177  
 Oy 185 GSSSHDTICTSCGTG 198  
 Db 178 -YPVNETSCRTTAG 190

RESULT 9  
 I37552  
 OX40 homolog - human  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
 C:Accession: I37552  
 R:Latza, U.; Durkop, H.; Schiltger, S.; Ringeling, J.; Eltelbach, F.; Hummel, M.; Fo  
 Eur. J. Immunol. 24, 677-683, 1994  
 A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen  
 A:Reference number: I37552; MUID:94170844  
 A:Accession: I37552  
 A:Status: preliminary; translated from GB/EMBL/DDHJ  
 A:Molecule type: mRNA  
 A:Residues: 1-277 <RES>  
 A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:9472958  
 C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 13.8%; Score 226; DB 2; Length 277;  
 Best Local Similarity 27.0%; Pred. No. 6.6e-10;  
 Matches 80; Conservative 25; Mismatches 117; Indels 74; Gaps 12;  
 Oy 6 GPELSLCLVIALPALLPVAVGVAEPTPYPMRDAETGERLVCAOCPGPTFVORPCRRD 65  
 Db 11 GPVALLLGLIGISTVGTGHCY-----GDTYPSNR-----CCHCKRGMNWSRCSRS 59  
 Oy 66 SPTTCGCPRRHYTOFWNY--LERCYCNVLCGEREEBARACHATNRCRRTGFEFAHA 123  
 Db 60 QNTVCRPCGPGGYNDVSSKPKPCTWNLIRSG--SERKOLATATQDVCRCRAG----- 112



```

OY 124 GFCLEHACSPGAGVIATAGTSPQNTQQOCPCPGFSSASSSSSECCQPHRNTALGALNV 183
Db 113 --TPLDLSTYKRG-----VDCAPCPGHP--SPGDNOACKPWNTCTLAGKHTLQ 156
OY 184 PCSSSHDPLCTS--CTGFPLSTRVPGCAEECEKRAVIDFVAFQDISIKRLQRLQALEAPE 240
Db 157 PASNSSDAICEDRDPPATNPQETQGPAPRI-----TVQPTG 193
OY 241 GW----GPRPR----AGRAALQLKRLRLTELLGAODGALLVRLQLQALRVAMP 286
Db 194 AMPRTSGPSPTRPEVPGSGRAVAATILGLVLGLGPL--ATLLALYLRLRDQRUP 247

RESULT 10
GQVZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: A40566
R:Upton, C.; Maceo, J.L.; Schreiber, M.; McFadden, G.
Virology 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A:Reference number: A40566; MUID:91335768
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <UTP>
A:Cross-references: GB:995181; GB:M37976; NID:9332309; PIDD:AAAA6632.1; PUD:9332310
C:Superfamily: Myxoma virus T2 protein; NGF receptor repeat homology
C:Keywords: glycoprotein
E:64-105/Domain: NGF receptor repeat homology <NG2>
E:106-147/Domain: NGF receptor repeat homology <NG3>
E:166,181,205,338/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match      13.2%  Score 215; DB 1; Length 326;
Best Local Similarity 29.38; Pred. No. 5,1e-09;
Matches 58; Conservative 22; Mismatches 96; Indels 22; Gaps 5;

OY      12 LCLVLPALL-----PPPAVRGVAEPTPTYPWRDAEGERLVCACCPGPFVGRCRDS 66
      | : : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      4 LTLILYVACYVGGGAPFGADRGKCRGNDY-----EKDGLCTISCPGGSVASKLCPGS 57

OY      67 PTTGCPCEPRHYTOFMWYLERCYRCNVLCGEREEARCAHATNHRACRRTGFEA----- 121
      | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db      58 DTVCSPCKNEFTASTFNHAPACVSCRGKCTGHLSESGCKDTRDVCDSAGNYCLKQG 117

OY      122 -HAGCLEHASCSPGAGYIACGPSQNTQCPCCPGPFSSASSSSBOCPHRNCTALGIA 180
      | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db      118 EGCRIACPKTKCPAGYGV-SGHTRTGDVLCIKCPRYTSDAVSSTETCTSSFNYSVEFN 176

OY      181 LNVGSSSHDPLCTSCCTG 198
      | : | : | : |
Db      177 L-----YPVNDTSCITTYAG 190

RESULT 11
S12783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12783; S08036
R:Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
A:Reference number: S12783; MUID:90214614
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C:Superfamily: CD27 antigen; NCF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
C:1-19/Domain: signal sequence #status predicted <Sig>

```

F:210-271/Product:	Ox40 antigen	#status predicted <MAT>
F:211-235/Domain:	transmembrane	#status predicted <TM>

  

Query Match	13.1%	Score 214;	DB 2;	Length 271;
Best Local Similarity	30.1%;	Pred. No. 5.1e-09;		
Matches	58;	Conservative	23;	Mismatches 64;
				Indels 48;
				Gaps
QY	10 SLILCVIALPALPLVPPAVRGVAETPTYPWRDPAEDGEBRLVCAOCPPGFVFVOPCRDRSPPT	69		
Db	10 AFLLLGLSLGTATLNCVK-----DYTP-----SGHR--CCRECPGHGMYSRCDHTRDIY	58		
QY	70 GCGPCPPIHYTFQFMY--LERCRYCNVLGCHEEERARACHATHNRACRTGFFAHAGFCL	127		
Db	59 CHPCPGPYNEAUVNDYCKCCTQCENHRSG--SELKNQCTPLETDIVGCCR-----	105		
QY	128 EHASCPRGAGVIACGT-PQSQT-----QCQPCPGTIFFSASSSSSECCQDPHRNCTALGIA	180		
Db	106 -----PGTOPRODSHHKLDCVPCCPPGHF--SPGSNQACKPMWNTCTLISGKO	150		
QY	181 LNVPGSSSHDFLC	193		
Db	151 IRRPASNSLDIVC	163		

Query Match	12.9%	Score 211	DB 2	Length 277
Best Local Similarity	30.5%	Pred. NO. 8.8e-09		
Matches 46	Conservative 21	Mismatches 76	Indels 8	Gaps 3
49 CAACPGFTFVQPCRRDPSPTTCGCPRPRIHYQFNMYLERC---RYCNVLGSEEREERARAC 105				
Db CSIQCPGGKIVSDCTEFRETETCLPQCSSEFLDWMNRETHGHQHKYCDPNGLRYQNGSTS 97				
QY 106 HATNNRACRTGTFPAHA---GFLIEHASCPRGACVILAGTPSPONTCCQPCPCTBSASS 162				
Db 98 ET-DTITCEEGMHTCSSEACSCVLHRSQSPGIVQVQITGVSDTICEPCPVGFENVS 155				







```

Db      10 LFLGALRAFPQDRPFDTCNGNPSHY---DKAVRRCYRCPMGLFTIQQCPQ-RPTDC 65
QY      71 -GPCPPRHYYTOFWNVLERCRCYNVLCGERE-EEARACHATHNRACRORTGFFAHAGF--- 125
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      66 RKQCEPDYTL---DEADRCTAC-VTCSRDDLVEKTPCAMNNSRVCCECRGMECSTSAVNS 121
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      126 ---CLEHASCPPGAGVIAPCTPSQNTQCPQCPGTFSSASSSSSECCQ-----PHRNCT 175
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      122 CARCFHSHVCPAGMIVKFPGTAKNTVCEPASBGV-SPACASPENCKEPSSGTIPQAKPT 180
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      176 ALGLALNVPSSSHDTL 192
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 PVS-----PATSSASTM 192
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: October 31, 2001, 12:39:33  
 Job time: 162 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2001, 12:39:12 ; Search time 10.26 Seconds

(without alignments)  
1001.622 Million cell updates/sec

Title: US-09-006-352-2

Perfect score: 1634

Sequence: 1 MRALEGPGLSLCLVLAIPA.....RVARNPGLERSVREPLPVH 300

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	353.5	21.6	461	TNR2_HUMAN	P20333 homo sapien
2	332.5	20.3	474	TNR2_MOUSE	P25119 mus musculu
3	315	19.3	435	TNR2_HUMAN	P36941 homo sapien
4	277	17.0	415	TNR2_MOUSE	P50284 mus musculu
5	262.5	16.1	349	VC22_VARV	P34015 varitola vir
6	236.5	14.5	325	VT2_SEVKA	P25943 shope fibro
7	226	13.8	277	OX40_HUMAN	P43489 homo sapien
8	215	13.2	326	VT2_MYXYL	P29825 myxoma viru
9	214	13.1	271	OX40_RAT	P15725 rattus norv
10	211	12.9	277	CD40_HUMAN	P25942 homo sapien
11	203	12.4	289	CD40_MOUSE	P27512 mus musculu
12	202	12.4	269	CD40_BOVIN	Q28203 bos taurus
13	198.5	12.1	272	OX40_MOUSE	P47741 mus musculu
14	186.5	11.4	256	CD30_HUMAN	P28908 homo sapien
15	185	11.3	255	41BB_MOUSE	P20334 mus musculu
16	176	10.8	416	NGFR_CHICK	P18519 gallus gall
17	175.5	10.7	427	NGFR_HUMAN	P08138 homo sapien
18	174	10.6	255	41BB_HUMAN	Q07011 homo sapien
19	170	10.4	425	NGFR_RAT	P07174 rattus norv
20	163	10.0	332	FASN_PIG	O77336 sus scrofa
21	160.5	9.8	471	TNR1_BOVIN	O19131 bos taurus
22	155.5	9.5	260	CD27_HUMAN	P26842 homo sapien
23	155.5	9.5	327	FASN_MOUSE	P25446 mus musculu
24	155	9.1	323	FASN_BOVIN	P51667 bos taurus
25	148	9.1	250	CD27_MOUSE	P41272 mus musculu
26	145	8.9	335	FASN_HUMAN	P25445 homo sapien
27	144	8.8	324	FASN_RAT	O63199 rattus norv
28	137.5	8.4	454	TNR1_MOUSE	P25118 mus musculu
29	129.5	7.9	1877	PCMS_MOUSE	Q04592 mus musculu
30	128.5	7.9	417	WSL1_HUMAN	Q93038 h wsl-1 pro
31	128.5	7.9	365	LMA5_MOUSE	O61001 mus musculu
32	127	7.8	1192	LMG2_MOUSE	O61092 mus musculu
33	125.5	7.7	461	TNR1_RAT	P22934 rattus norv

34	125.5	7.7	1255	1	ERB2_HUMAN	P04626 homo sapien
35	124.5	7.6	1696	1	PCMS_BRACL	Q9n15 brachiosto
36	124.5	7.6	1713	1	LMA3_HUMAN	Q16787 homo sapien
37	124.5	7.6	3106	1	LMA2_MOUSE	Q06675 mus musculu
38	123.5	7.6	455	1	TNR1_HUMAN	P19438 homo sapien
39	123.5	7.6	2813	1	VWF_CANPA	Q28395 canis famli
40	123	7.5	2569	1	LMA3_MOUSE	Q61789 mus musculu
41	120	7.3	1609	1	LMG1_HUMAN	P11047 homo sapien
42	119.5	7.3	2318	1	NTC3_MOUSE	Q61982 mus musculu
43	119.5	7.3	461	1	TNR1_PIG	P50555 sus scrofa
44	119.5	7.3	3084	1	LMA1_MOUSE	P19137 mus musculu
45	118.5	7.3	1680	1	FUR2_DROME	P30432 drosophila

## ALIGNMENTS

RESULT	ID	TNR2_HUMAN	STANDARD	PRT	461 AA.
AC	P20333				
DT	01-FEB-1991	(Rel. 17, Created)			
DT	01-AUG-1991	(Rel. 19, Last sequence update)			
DT	01-OCT-2000	(Rel. 40, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TNFRI) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).				
GN	TNFRSF1B OR TNFR2 OR TNFR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90260639; PubMed=2160731;				
RA	Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,				
RA	Dower S.K., Cosman D., Goodwin R.G.,				
RT	"A receptor for tumor necrosis factor defines an unusual family of				
RT	cellular and viral proteins.";				
RL	Science 248:1019-1023(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91045991; PubMed=2172983;				
RA	Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,				
RA	Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.,				
RT	"A second tumor necrosis factor receptor gene product can shed a				
RT	naturally occurring tumor necrosis factor inhibitor.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96299745; PubMed=8661109;				
RA	Bellinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,				
RA	Lepallier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,				
RT	Brodeur G.M.;				
RL	"Physical mapping and genomic structure of the human TNFR2 gene.";				
RL	Genomics 35:94-100(1996).				
RN	[4]				
RP	SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.				
RX	MEDLINE=90349572; PubMed=2166946;				
RA	Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,				
RA	Ringold G.M.;				
RT	"Complementary DNA cloning of a receptor for tumor necrosis factor				
RT	and demonstration of a shed form of the receptor.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).				
RN	[5]				
RP	SEQUENCE OF 27-31.				
RX	MEDLINE=90110215; PubMed=2153136;				
RA	Engelmann H., Novick D., Wallach D.;				
RT	"Two tumor necrosis factor-binding proteins purified from human				
RT	urine. Evidence for immunological cross-reactivity with cell surface				
RT	tumor necrosis factor receptors.";				
RL	J. Biol. Chem. 265:1531-1536(1990).				
RN	[6]				
RP	SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.				



RA MEDLINE-91056048; PubMed-2173696;  
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brockhaus M.;  
 RA "Purification and partial amino acid sequence analysis of two  
 RT distinct tumor necrosis factor receptors from HL60 cells.";  
 RT J. Biol. Chem. 265:20131-20138(1990).  
 [7]  
 RP CHARACTERIZATION:  
 RA MEDLINE-93016040; PubMed-1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor  
 RT phosphorylation.";  
 RT J. Biol. Chem. 267:21172-21178(1992).  
 RL (8)  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
 RP MEDLINE-99221490; PubMed-10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of  
 RT human TRAF2.";  
 RT Nature 398:533-538(1999).  
 RL Nature 398:533-538(1999).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND  
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 CC LEVEL ON THREONINE RESIDUES.  
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND  
 CC WEETH-AVERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID  
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING  
 CC PORTION OF TNFR1 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO  
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS A IA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD120b entry.  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm"  
 CC -1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;  
 CC WWW="http://www.enbrelinfo.com/"  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation-  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; M32315; AAA59929.1; -;  
 DR EMBL; M35857; AAA63462.1; -;  
 DR EMBL; U52165; AAC50622.1; JOINED.  
 DR EMBL; U52156; AAC50622.1; JOINED.  
 DR EMBL; U52157; AAC50622.1; JOINED.  
 DR EMBL; U52158; AAC50622.1; JOINED.  
 DR EMBL; U52159; AAC50622.1; JOINED.  
 DR EMBL; U52160; AAC50622.1; JOINED.  
 DR EMBL; U52161; AAC50622.1; JOINED.  
 DR EMBL; U52162; AAC50622.1; JOINED.  
 DR EMBL; U52163; AAC50622.1; JOINED.  
 DR EMBL; U52164; AAC50622.1; JOINED.  
 DR EMBL; M55994; AAA36755.1; JOINED.  
 DR PIR; A35366; A35366.  
 DR PIR; A36007; A36007.  
 DR PIR; A36475; A36475.  
 DR PIR; B35010; B35010.  
 DR PIR; A23666; A23666.  
 DR PDB; 1CA9; 12-APR-99.  
 DR MIM; 191191; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 4.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 KW Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 22

FT CHAIN 23 461  
 FT DOMAIN 23 257  
 FT TRANSMEM 258 287  
 FT DOMAIN 288 461  
 FT DOMAIN 39 201  
 FT REPEAT 39 76  
 FT REPEAT 77 118  
 FT REPEAT 119 162  
 FT REPEAT 163 201  
 FT DISULFID 40 53  
 FT DISULFID 54 62  
 FT DISULFID 57 75  
 FT DISULFID 78 93  
 FT DISULFID 96 110  
 FT DISULFID 100 118  
 FT DISULFID 120 126  
 FT DISULFID 134 143  
 FT DISULFID 137 161  
 FT DISULFID 164 179  
 FT CARBOHYD 171 193  
 FT CARBOHYD 193 193  
 FT CONFLICT 141 141  
 FT CONFLICT 141 141  
 FT CONFLICT 196 196  
 FT CONFLICT 363 363  
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;  
 Query Match 21.6%; Score 353.5; DA 1; Length 461;  
 Best Local Similarity 29.8%; Pred No 8.2e-21;  
 Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;  
 QY 8 GLSLICLVLPALPVPVAVRVAETPTVYWRDAE-----RLYACQCPG 55  
 DB 13 GLELMAAALP-----QVAFPIAP-----EGSCRLREYDDOTAKCCSCSPG 60  
 QY 56 TVVQPCRDSPPTGCPGPRHYTQFWNLERCRCYNVLGCEEREARACHATNPRAC 115  
 DB 61 QHAKVFCTKSDTVVCDSCEDSTYTLQMLNVPETCLSGKSSDDVOTACTREONNICTG 120  
 QY 116 RTGFPAHAG-----FLEHASCPCGAYIAPGTPSONTOCPGPTFSASSSSDQO 169  
 DB 121 RPYWCALSKQECRCRCAPLRKCRPGVAPGTETSDVVCRCAPGTFSNTSSDTCR 180  
 QY 170 PHNCTALGIALVWPSSSHDTLCTCTGPTLSTRVGAEECEERAVIDVAFODISIKRL 229  
 DB 181 PQCICNVVA-----IPGASRADVACTST--PTRSMAFGAVHLEQV-----STRSQT 227  
 QY 230 QRLQALEAPE-----GMGPTPRA-----GRALQLKLRRLTFLGAQDGLVRLQL 280  
 DB 228 QPTPEPSTASTSFLPLPMGSPFPAESGTDFALPVGLIYGTAL-----GLIIGVNCV 282  
 QY 281 ---RYVAMP--GLERSVRERLP 298  
 DB 283 IMTVKKKPLCLQREAKVPLP 304  
 RESULT 2  
 TNFR\_MOUSE STANDARD: PRT: 474 AA.  
 ID TNFR\_MOUSE  
 AC P25119; P97893;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).  
 GN TNFRSF1B OR TNFR2 OR TNFR-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC Nobi; Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91187885; PubMed-1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,



20.38; Score 332.5; DB 1; Length 474;

```

Best Local Similarity 29.7%, Pred.No.3.7e-19;
Matches 81, Conservative 44, Mismatches 109; Indels 39; Gaps 9;

OY      46 RLVAQCEPGRPTFYVPCRRDSTTGPPCPRIITYTFNNYLECRICNVLCGEREEAARAC 105
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       52 OMCAKACEPGGVYVKHFCKNKTSDTYCADCEASMYIVVMNQFRTCLSSSCSTDTDYETIRAC 111
OY      106 HATHRARCRRTGFE-----AHAGF---CLEHAQSPGAGVIAPRPSNTQCOPPCPGFF 158
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       112 TKQQRVACAGEGRCAIKTKTHSGRCQCMRLSKCGPFGVASSRAPGNVLCKAAAPGT 171
OY      159 SASSESSQCCOPPHRNCTALGLANPCSSSHDTLCT----SCTGPPLSYRYVGAECERA 214
          |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       172 SDTTSSTDVCNRHRICSLIA-----IPGASNDVACAPESPTLSALPRLLYVSQPEPTSQ 227
OY      215 VIDVEAFDDISIKRLQLLQALEADEGMGPPD-----RAGRRAOLKLRRLTELLGAOD 269
          :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       228 PLD-----GEPPGSQPSILTSL-----GSMPIIQSTKGIGSLPIGLVGVTSL----- 272
OY      270 GALLVRLLOAL-----RVARMGLESVVERFLP 298
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       273 GLMLGLVNCIILVQRKKRPSCLDRAVPHPV 305

RESULT   3
TNRC_HUMAN TNRC_HUMAN STANDARD: PRT: 435 AA.
AC          P36941;
DT          01-JUN-1994 (Rel. 29, Created)
DT          01-JUN-1994 (Rel. 29, Last sequence update)
DT          01-OCT-2000 (Rel. 40, Last annotation update)
DE          LMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE          2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
EN          LITER OR TMFCR OR TNFRSF3.
OS          Homo sapiens (Human).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX          NCBI_TaxID=9606;
RN         [1]
RP         SEQUENCE FROM N.A.
RC         TISSUE=Liver;
RX         MEDLINE=93252381; PubMed=8486360;
RA         Baetis M., Chaffanet M., Cassiman J.J., den Bergh H., Marynen P.;
RT         "Construction and evaluation of a hmcDNA library of human l2p
RL         transcribed sequences derived from a somatic cell hybrid.";
RN         Genomics 16:214-218(1993).
RN         [2]
RP         FUNCTION.
RX         MEDLINE=94225209; PubMed=817123;
RA         Crowe P.D., van Arsdale T.U., Walter B.N., Ware C.F., Hession C.,
RA         Ehrenfelds B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT         "A lymphotoxin-beta-specific receptor.";
RL         Science 264:707-710(1994).
CC         -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC         IMMUNE DEVELOPMENT.
CC         -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC         -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
Cc         This SWISS-PROT entry is copyright. It is produced through a collaboration
Cc         between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Cc         use by non-profit institutions as long as its content is in no way
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Cc         entities requires a license agreement (see http://www.isb-sib.ch/announce/
Cc         or send an email to license@isb-sib.ch).
Cc         -----
DR         EMBL: U04270; AAA36757.1; -.
DR         HSSP: P25942; ICDF.
DR         MIM: 600979; -.
DR         InterPro: IPR001368; -.
DR         Pfam: PF00020; TNFR_C6; 4.
DR         ProSITE: PS00652; TNFR_NGFR_1; 2.
DR         ProSITE: PS00050; TNFR_NGFR_2; 3.

```



KW Receptor; Transmembrane; Glycoprotein; Repeat; signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 435  
 FT DOMAIN 31 227  
 FT TRANSMEM 228 248  
 FT DOMAIN 249 435  
 FT DOMAIN 442 211  
 FT REPEAT 42 81  
 FT REPEAT 82 124  
 FT REPEAT 125 168  
 FT REPEAT 169 211  
 FT DISULFID 59 72  
 FT DISULFID 62 80  
 FT DISULFID 83 98  
 FT DISULFID 101 116  
 FT DISULFID 104 124  
 FT DISULFID 126 132  
 FT DISULFID 139 148  
 FT DISULFID 142 167  
 FT DISULFID 170 185  
 FT CARBOHYD 40 40  
 FT CARBOHYD 177 177  
 SQ SEQUENCE 435 AA; 46709 MW; 62462656022F56F CRC64;

Query Match 19.3%; Score 315; DB 1; Length 435;  
 Best Local Similarity 31.8%; Pred. No. 8.1e-18;  
 Matches 89; Conservative 29; Mismatches 120; Indels 42; Gaps 12;

OY 3 ALEPGSLICLVLPALPVPVAVGVAETPTV-----FMRDA-----ETGERLYCAQC 52  
 DB 6 ATAPAGLWGLVGLGLGLLAASQPAV---PAYASENQCRDQEKRYEPQHICCSRC 62  
 OY 53 PPGTFVQRPGRDPTTCGPRPRHYQFVNYL---ERCRCYVLCGEREEREAACHATH 109  
 DB 63 PPGTYVNAKSRIDYCAITCAENSYNEHNNYLTICQLCRCDVYMG--LEETAPCTSKR 120  
 OY 110 NRACRCRTGFFAHAGFCLE--H-----ASCPRGA-GVIAIPCTPSQNTCCQPCPTGSASS 162  
 DB 121 KTCRCQCGMFC-AAMALECTHELSDCPGTAEALIKDEYGNKNNCVCKRACHFQNTS 179  
 OY 163 SSQSCOPHNRCTALGLALNPGSSSHDPLCTCTGTFPLSTRVPGAECEERAVIDEVAFQ 222  
 DB 180 SPASRCQPHRCENQGLVEAPGTAQSDITCKNPLE-PLPEMSTMLMLAVLPIAFL 238  
 OY 223 DIS-----TKRLQRLQALEAPGCMGPTPRAG 249  
 DB 239 LLATVFSCIMKSHPSLCKRLGSLK--RRQEGSPNPVAG 276  
 RESULT 4  
 TNRC MOUSE STANDARD; PRT; 415 AA.  
 AC P50284;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.  
 GN LTBR OR TNFR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX STRAIN=CVB; TISSUE=Lung;  
 RX MEDLINE=96072804; PubMed=7594541;  
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,  
 RA Browning J.L., Ware C.F.;  
 RA "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,  
 RT and expression.";  
 RL J. Immunol. 155:5280-5286(1995).

RN SEQUENCE FROM N.A.  
 RA MEDLINE=96163885; PubMed=8586432;  
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,  
 RA Honjo T.;  
 RA "The murine lymphotoxin-beta receptor cDNA: isolation by the signal  
 RT sequence trap and chromosomal mapping.";  
 RL Genomics 30:312-319(1995)  
 CC - FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC - IMMUNE DEVELOPMENT.  
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; U29173; AAA8964.1; -  
 DR EMBL; L38423; AAB00846.1; -  
 DR EMBL; U30798; AAB1334.1; -  
 DR HSSP; P25942; ICDF.  
 DR MGD; MGI:104875; Ltbr.  
 DR InterPro; IPR001368; -  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR ProSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR ProSITE; PS50050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 415  
 FT DOMAIN 31 223  
 FT TRANSMEM 224 244  
 FT DOMAIN 245 415  
 FT DOMAIN 42 213  
 FT REPEAT 42 81  
 FT REPEAT 82 124  
 FT REPEAT 125 170  
 FT REPEAT 171 213  
 FT DISULFID 43 58  
 FT DISULFID 59 72  
 FT DISULFID 62 80  
 FT DISULFID 83 98  
 FT DISULFID 101 116  
 FT DISULFID 104 124  
 FT DISULFID 126 132  
 FT DISULFID 139 150  
 FT DISULFID 142 169  
 FT DISULFID 172 187  
 FT CARBOHYD 40 40  
 FT CARBOHYD 179 179  
 SQ SEQUENCE 415 AA; 44956 MW; 29B32656A6E661 CRC64;

Query Match 17.0%; Score 277; DB 1; Length 415;  
 Best Local Similarity 31.2%; Pred. No. 7.4e-15;  
 Matches 88; Conservative 29; Mismatches 105; Indels 60; Gaps 14;  
 OY 6 GP-----GLSLICLVLPALPVPVAVGVAETPTVPRDAETGERL---VCAOCPPGTQV 59  
 DB 15 GPLLLICSLGL-LVASPOLVPPVRL-----ENQICWQDDEYEPHMDVCCSPGPEVFF 69  
 OY 60 RPCRSDPTTCGPRPRHYQFVNYL---ERCRCYVLCGEREEREAACHATHNACR 116  
 DB 70 AVCSRQSDVYCKTCPRHNSYNEHNNHLSCTCLCPICIVLG--FEETAPCTSRKAECRCQ 127  
 OY 117 TGFFAHAGFCLE---SHASCPAGVIA-PGTPSNT-----OCQCPGPTGSASS 163  
 DB 128 PGM-----SCVYIDNCCVHCERELVLCOPGTAEAVTDEIMTDVAVCVCKRGHFNQNTS 182  
 OY 164 SSQSCOPHNRCTALGLALNPGSSSHDPLCTCTGTFPLSTRVPGAECEERAVIDEVAF-- 221



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Db 183 PRACOPHTRCEIQLGVEAAGTSTSYDTC-----NPEPGAMLLAILSLVLELL 235
OY 222 -----ODISIKRLQRLQLEAPEGWG-----PTPRA 248
Db 236 FTTVLACAMWHRHPSLCRKIGTLLK--RHPEGEESPPOCAPRA 275

RESULT 5
VC22_VARY STANDARD: PRT: 349 AA.
ID VC22_VARY
AC P34015:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROTEIN C22/B28 HOMOLOG.
GN G4R.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-INDIA-1967 / ISOLATE IND3;
RX MEDLINE-93202281; PubMed-8364129;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms."
RL FEBS Lett. 319:80-83(1993).
CC -1- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X69198; CAA49137.1; -
CC EMBL: X67117; CAA47540.1; -
CC PIR: D36858; D36858.
CC PIR: S35987; S35987.
CC PIR: S46888; S46888.
CC HSSP: P19438; 1NCR.
CC InterPro: IPR001368; -.
CC Pfam: PF00020; TNFR_C6; 2.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS50050; TNFR_NGFR_2; 2.
CC Repeat.
CC KW DOMAIN 31 108 2 X TNFR-CYS.
CC REPEAT 31 66 TNFR-CYS 1.
CC REPEAT 67 108 TNFR-CYS 2.
CC FT REPEAT
CC FT REPEAT
CC SQ SEQUENCE 349 AA; 38189 MW; D45040B5C6E780EF CRC64;

Query Match 16.1%; Score 262.5; DB 1; Length 349;
Best Local Similarity 30.0%; Pred. No. 8,6e-14;
Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;
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```
Db 183 ITLYPVNDTSCRTTGTGISEIITSE 209
RESULT 6
VT2_SFVKA STANDARD: PRT: 325 AA.
ID VT2_SFVKA
AC P25943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10272;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91207415; PubMed-2820128;
RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RT telomeric region of the Shope fibroma virus genome.";
RL Virology 160:20-30(1987).
RN [2]
RP FUNCTION.
RX MEDLINE-91207415; PubMed-1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
RT form of the TNF receptor.";
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPEINING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
CC EMBL: M17433; -; NOT ANNOTATED_CDS.
CC EMBL: A23727; CAA01687.1; -
CC PIR: B43692; B43692.
CC HSSP: P19438; 1TNR.
CC InterPro: IPR001368; -.
CC Pfam: PF00020; TNFR_C6; 2.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS50050; TNFR_NGFR_2; 1.
CC KW Receptor; Glycoprotein; Repeat; Signal.
CC FT SIGNAL 1 16
CC FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
CC FT DOMAIN 27 186 4 X TNFR-CYS.
CC FT REPEAT 27 62 TNFR-CYS 1.
CC FT REPEAT 63 104 TNFR-CYS 2.
CC FT REPEAT 105 147 TNFR-CYS 3.
CC FT REPEAT 148 186 TNFR-CYS 4.
CC FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 325 AA; 35132 MW; 81053039198A71E CRC64;

Query Match 14.5%; Score 236.5; DB 1; Length 325;
Best Local Similarity 29.9%; Pred. No. 8,8e-12;
Matches 58; Conservative 25; Mismatches 94; Indels 17; Gaps 4;
```



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Db 8 LVCVVYVYDGVDPVSSNGKCGHDY-----EKDGLCCASCHGFAVSRCLGPGSNTVC 61
Oy 71 GPCPRHYTOFMNYLERCRYCNVLCGEREEARACHATHNRACRRTGFFA-----HAG 124
Db 62 SPCEGDTFTASTNHAPACVSCRCGPTGHLSESOPCDRHDVNCSTGNCYLTKGONCR 121
Oy 125 FCLFHASCPGAGVYAPCTPSQNTQCPCPGTFSSASSSSSEOCOPHRNCALGLALNV 184
Db 122 ICAPQTKCPAGYGV-SGHTRADGLCEKCPPHYSDLSLPTERCSTPNYISVGFNL--- 177
Oy 185 GSSSHDTLCTSCQT 198
Db 178 -YPVNETSCTTATAG 190

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## RESULT 7

OX40 HUMAN STANDARD: PRT: 277 AA.

```

AC P43489.013663.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
GN TNFRSF4 OR TXGP1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP MEDLINE=94170844; PubMed=7510240;
RX Latza U., Duerkop H., Schultze S., Ringeling J., Eitelbach F.,
RA Hummel M., Fonatsch C., Stein H.;
RT "The human OX40 homologue: cDNA structure, expression and chromosomal
RT assignment of the ACT35 antigen."
RL Eur. J. Immunol. 24:677-683(1994).
[2]
RN 12
RP MEDLINE=95219871; PubMed=7704935;
RX Baum P.R., Gayle R.B., III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA Watson M., Sedlin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT "Identification of OX40 ligand and preliminary characterization of
RT its activities on OX40 receptor."
RL Cite. Shock 44:30-34(1994).

```

```

CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD134 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".

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DR EMBL; X75962; CAAS3576.1; -
DR EMBL; S76792; AAB33944.1; ALT_INIT.
DR HSSP; P25942; ICDF.
DR MIM; 600315; -
DR InterPro; IPR001368; -
DR Pfam; PF000020; TNFR_C6_3
DR PROSITE; PS00652; TNFR_NGFR_1_3
DR PROSITE; PS00500; TNFR_NGFR_2_2
DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KM Signal.
FT SIGNAL 1 28
FT CHAIN 29 277 POTENTIAL.
FT DOMAIN 29 214 OX40L RECEPTOR.
FT EXTRACELLULAR (POTENTIAL).

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```

FT TRANSMEM 215 235
FT DOMAIN 236 277 POTENTIAL.
FT DOMAIN 30 169 CYTOPLASMIC (POTENTIAL).
FT REPEAT 30 65 4 X TNFR-CYS.
FT REPEAT 66 107 TNFR-CYS 1.
FT REPEAT 108 126 TNFR-CYS 2.
FT REPEAT 127 167 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 146 166 TNFR-CYS 4.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

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Query Match 13.8%; Score 226; DB 1; Length 277;  
Best local Similarity 27.0%; Pred. No. 56-11; Indels 74; Gaps 12;  
Matches 80; Conservative 25; Mismatches 117;

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Oy 6 GPGISLLCLVLAIPALIPVAVGVAFETPYPRDAETGERLYCAACPPTGVQPRCD 65
Db 11 GPCALALLGLGLSTVYGLHCY-----GDYPSNDR-----CHCECRGNGVSRCSRS 59
Oy 66 SPTTGPCCPRHYTOFMN--LERCRYCNVLCGEREEARACHATHNRACRRTGFFAHA 123
Db 60 QNTVCRGCGGFYNDVSSKRCPCRCWMLRSG--SERKOLCTATQDTCRCRAG----- 112
Oy 124 FCLFHASCPGAGVYAPCTPSQNTQCPCPGTFSSASSSSSEOCOPHRNCALGLALNV 183
Db 113 -TOPLEDSYKRG-----VDCAPCPGHF--SPGDONQCKPWNCTLAGKHRLQ 156
Oy 184 PGSSSHDTLCTSCQT-----CTGPPLSTRVPGAECECERAVIDFAFODISIKRLQLQLALEAVE 240
Db 157 PASNSDIALCEDRDPPATQFOETGPPAPRI-----TVQPT 193
Oy 241 GW-----GPTPR-----AGRAALQLKRRRLTELGADGALVRLQLARVAMP 286
Db 194 AMPTSGPSTREVEYVPGRAVAIIIGLVIGLTLPL--ALLALVTLRRQGRLEP 247

```

## RESULT 8

VT2 MYXVL STANDARD: PRT: 326 AA.

```

ID VT2_MYXVL
AC P29825.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=31530;
RN 11
RP MEDLINE=9135768; PubMed=1651597;
RX Upton C., Maceo J.L., Schreiber M., McGadden G.;
RA "Myxoma virus expresses a secreted protein with homology to the tumor
RT necrosis factor receptor gene family that contributes to viral
RT virulence."
RL Virology 184:370-382(1991).

```

```

CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

```

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DR EMBL; M95181; AAA46632.1; -
DR EMBL; A23729; CAA01688.1; -

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DR PIR: A40566; GOVZML.  
DR HSSP: P19438; 1TNR.  
DR InterPro: IPR001368; .  
DR Pfam: PF00020; TNR\_C6; 2.  
DR PROSITE: PS00652; TNR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNR\_NGFR\_2; 2.  
DR Receptor: Glycoprotein; Repeat; Signal.  
KW SIGNAL.  
FT CHAIN 1 16 POTENTIAL.  
FT DOMAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.  
FT REPEAT 27 186 4 X TNR-CYS.  
FT REPEAT 27 62 TNR-CYS 1.  
FT REPEAT 63 104 TNR-CYS 2.  
FT REPEAT 105 147 TNR-CYS 3.  
FT REPEAT 148 186 TNR-CYS 4.  
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;

Query Match 13.2%; Score 215; DB 1; Length 326;  
Best Local Similarity 29.3%; Pred. No. 4.3e-10;

Matches 58; Conservative 22; Mismatches 96; Indels 22; Gaps 5;

QY 12 LCLVLAIPALP-----PVAVRGVAETPTYPWRDAETGERLVCACCPGTFVORPCRRDS 66  
DB 4 LTLALLVAVACVGGAGPYGADRGKRGNDY-----EKDGLCTSCPPGSYARLCLGPGS 57  
QY 67 PTTGCGPPRHATYQFNWNYLERCRYCNVLCGEREEBARACHATNNRACRGTGFA----- 121  
DB 58 DTVCSCKMKEFTASTNHPACVSCRGRCRGLSESOSCKTRDRVDCSAGNYCLIKGQ 117  
QY 122 -HAGFLEHASCPGAGVIAPGTPSONTCQCPGPTGFSASSSSSECCOPHRNCTALGLA 180  
DB 118 EGRICAPRTKCPAGYGV-SGHTRTGDVLCTKCPRTTSDAVSSTETCTSSFNIVSEFN 176  
QY 181 LNVPGSSSHDTLCTSCGT 198  
DB 177 L-----YFVNDSTCTTAG 190

RESULT 9  
OX40\_RAT  
ID OX40\_RAT STANDARD: PRT; 271 AA.  
AC P15725;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).  
GN TNFRSF4 OR TNFRP1 OR OX40.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=T-cell;  
RX MEDLINE=90214614; PubMed=2157591;  
RA Mallett S., Fossum S., Barclay A.N.;  
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T  
lymphocytes -- a molecule related to nerve growth factor receptor.";  
RL EMO J. 9:1063-1068(1990).  
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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DR EMBL: X17037; CA34897.1; .  
DR PIR: S08036; S08036.  
DR PIR: S12783; S12783.  
DR HSSP: P25942; 1CDF.  
DR InterPro: IPR001368; .  
DR Pfam: PF00020; TNR\_C6; 3.  
DR PROSITE: PS00652; TNR\_NGFR\_1; 3.  
DR PROSITE: PS50050; TNR\_NGFR\_2; 2.  
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
KW SIGNAL.  
FT CHAIN 1 19 POTENTIAL.  
FT DOMAIN 20 271 OX40L RECEPTOR.  
FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 211 235 POTENTIAL.  
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 164 4 X TNR-CYS.  
FT REPEAT 25 60 TNR-CYS 1.  
FT REPEAT 61 102 TNR-CYS 2.  
FT REPEAT 103 123 TNR-CYS 3 (INCOMPLETE).  
FT REPEAT 124 164 TNR-CYS 4.  
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 13.1%; Score 214; DB 1; Length 271;  
Best Local Similarity 30.1%; Pred. No. 4.3e-10;

Matches 58; Conservative 23; Mismatches 64; Indels 48; Gaps 9;

QY 10 SLCLVLAIPALPVPVAVRGVAETPTYPWRDAETGERLVCACCPGTFVORPCRRDSPTT 69  
DB 10 AFLGLGLSLGVTKLVKVK-----DTTP-----SGHK-CRCEQPGMGMSRCDHTRTDY 58  
QY 70 CGCPPPRHATYQFNWNYLERCRYCNVLCGEREEBARACHATNNRACRGTGFAHAGFCL 127  
DB 59 CHPCPEGFYNEAVNYDCKCTOCNHRSG--SELKONCTPEPTVCCR----- 105  
QY 128 EHASCPPGAGVIAPGT-PSONT-----OCQCPGPTGFSASSSSSECCOPHRNCTALGLA 180  
DB 106 -----PGTQPRDSSSHKLGVDVPCPPGHF--SPGSNACKPWTCTTSGKQ 150  
QY 181 LNVPGSSSHDTLC 193  
DB 151 IRRHPSNSIDTVC 163

RESULT 10  
CD40\_HUMAN  
ID CD40\_HUMAN STANDARD: PRT; 277 AA.  
AC P25942;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)  
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).  
GN TNFRSF5 OR CD40.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=89356608; PubMed=2475341;  
RX Stamenkovic I., Clark E.A., Seed B.;  
RT "A B-lymphocyte activation molecule related to the nerve growth  
factor receptor and induced by cytokines in carcinomas.";  
RL EMO J. 8:1403-1410(1989).  
CC [2]  
CC 3D-STRUCTURE MODELING OF 24-144.  
RP MEDLINE=97189482; PubMed=9037712;  
RA Bajorath J., Aruffo A.;



```

RT      "Construction and analysis of a detailed three-dimensional model of
        the ligand binding domain of the human B cell receptor CD40."
RN      Proteins 27:59-70(1997).
RP      [3]
RP      3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX      MEDLINE=98266353; PubMed=9605317;
RA      Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA      Zheng Z., Naismith J.H., Thomas D.;
RT      "The role of polar interactions in the molecular recognition of CD40L
        with its receptor CD40."
RL      Protein Sci. 7:1124-1135(1998).
CC      -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC      -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC      -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
        WWW=http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm"
CC      -----
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        or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X60592; CAA43045.1; -
DR      PIR; S04460; S04460.
DR      PDB; 1CDF; 01-APR-97.
DR      MIM; 109535; -
DR      InterPro; IPR001368; -
DR      Pfam; PF00020; TNFR.cf.4.
DR      PROSITE; PS00652; TNFR.NGFR.1; 1.
DR      PROSITE; PS50050; TNFR.NGFR.2; 4.
KW      Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW      3D-structure.
FT      SIGNAL                     1          19
FT      CHAIN                     20         277
FT      DOMAIN                    20         193
FT      TRANSMEM                  194        215
FT      TRANSEM                   216        277
FT      DOMAIN                    25         187
FT      DOMAIN                    25         60
FT      REPEAT                    61         103
FT      REPEAT                    104        144
FT      REPEAT                    145        187
FT      DISULFID                  26         37
FT      DISULFID                  38         51
FT      DISULFID                  41         59
FT      DISULFID                  62         77
FT      DISULFID                  83         103
FT      DISULFID                  105        119
FT      DISULFID                  111        116
FT      DISULFID                  125        143
FT      CARBOHYD                  153        153
FT      CARBOHYD                  180        180
SQ      SEQUENCE                     277 AA; 30619 MW; BC8776EC2CA45680 CRC64;

Query Match      12.9%; Score 211; DB 1; Length 277;
Best Local Similarity 30.5%; Pred. No. 7.5e-10;
Matches 46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;

DB      156 SAFKCHPWTSCETKDLVVOAGTNKTDVVC 186
RESULT 11
ID      CD40_MOUSE                 STANDARD;          PRT;          289 AA.
AC      P27512;
DT      01-AUG-1992 (Rel. 23, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).
GN      TNFRSF5 OR CD40.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92105763; PubMed=1370315;
RA      Torres R.M., Clark E.A.;
RT      "Differential increase of an alternatively polyadenylated mRNA
        species of murine CD40 upon B lymphocyte activation."
RL      J. Immunol. 148:620-626(1992).
RN      [2]
RP      REVISIONS.
RC      STRAIN-BALB/C;
RA      Torres R.M.;
RN      Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BALB/C; TISSUE=Liver;
RX      MEDLINE=93094586; PubMed=1281194;
RA      Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA      Howard M., Cockayne D.A.;
RT      "Genomic structure and chromosomal mapping of the murine CD40 gene."
RL      J. Immunol. 149:3921-3926(1992).
CC      -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC      -----
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CC      -----
DR      EMBL; M8312; AAB08705.1; -
DR      EMBL; M94126; AAA37404.1; -
DR      EMBL; M94129; AAA37404.1; JOINED.
DR      EMBL; M94128; AAA37404.1; JOINED.
DR      EMBL; M94127; AAA37404.1; JOINED.
DR      PIR; A46476; A46476.
DR      HSSP; P25942; 1CDF.
DR      MGD; MGI:88336; TNFRSF5.
DR      InterPro; IPR001368; -
DR      Pfam; PF00020; TNFR.cf.4.
DR      PROSITE; PS00652; TNFR.NGFR.1; 1.
DR      PROSITE; PS50050; TNFR.NGFR.2; 4.
KW      Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW      SIGNAL                     1          19
KW      CHAIN                     20         289
KW      DOMAIN                    20         193
KW      TRANSEM                   216        277
KW      TRANSEM                   25         187
KW      DOMAIN                    25         60
KW      REPEAT                    61         103
KW      REPEAT                    104        144
KW      REPEAT                    145        187
KW      CARBOHYD                  153        153
SQ      SEQUENCE                     289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

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DR	PROSITE: PS50050: TNFR, NFR, 2.2.	
KW	Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;	
KW	SIGNAL.	
FT	SIGNAL.	1
FT	CHAIN	20
FT	DOMAIN	272
FT	DOMAIN	20
FT	TRANSMEM	211
FT	DOMAIN	236
FT	DOMAIN	237
FT	DOMAIN	272
FT	DOMAIN	26
FT	REPEAT	165
FT	REPEAT	61
FT	REPEAT	26
FT	REPEAT	62
FT	REPEAT	103
FT	REPEAT	104
FT	REPEAT	124
FT	REPEAT	125
FT	CARBOHYD	144
FT	CONFLICT	144
FT	SEQUENCE	15
SO	272 AA; 3015 MW; 06B7B6415670D08E CRC64;	

RX	MEDLINE-96437016; PubMed-8839832.
RA	Hortle R., Ito K., Talewami M., Nagai M., Aizawa S.,
RB	Nishigahara M., Ishida T., Inoue J., Takizawa H., Watanabe T.:
RT	"A variant C30J protein lacking extracellular and transmembrane domain
RT	is induced in HL-60 by tetradecanoylphorbol acetate and is expressed
RL	in alveolar macrophages.";
CC	Blood 88:2422-2432(1996).
CC	- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD30L. MAY PLAY
CC	A ROLE IN THE REGULATION OF CELLULAR GROWTH AND TRANSFORMATION OF
CC	ACTIVATED LYMPHOBLASTS. REGULATES GENE EXPRESSION THROUGH
CC	ACTIVATION OF NFkB.
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	- ALTERNATIVE PRODUCTS: A SHORTER CYTOPLASMIC FORM C30V WHICH IS
CC	ONLY EXPRESSED IN ALVEOLAR MACROPHAGES IS PRODUCED BY THE USE
CC	OF AN ALTERNATIVE INITIATION CODON IN THE SAME READING FRAME.
CC	- PTM: PHOSPHORYLATED ON SERINE AND TYROSINE RESIDUES.
CC	- DISEASE: MOST SPECIFIC HOGKIN'S DISEASE ASSOCIATED ANTIGEN.
CC	- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC	- DATABASE: NAME=PROW; NOTE=Cd guide C30J entry;
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd30.htm".
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	entities requires a license agreement (See http://www.isb-sib.ch/annouce/
CC	or send an email to licenses@isb-sib.ch).
DR	EMBL; M83554; AAA51947.1; -
DR	EMBL; S75768; AAD14186.1; -
DR	EMBL; D86042; BAA12973.1; -
DR	PIR; A42086; A42086.
DR	HSSP; P19438; INCF.
DR	MIM: 153243; -
DR	InterPro: IPRO01368; -
DR	Pfam: PF00020; TNFR_c6; 4.
DR	PROSITE: PS00652; TNFR_NGFR.1; 2.
DR	PROSITE: PS00050; TNFR_NGFR.2; 2.
KW	T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;
KW	Phosphorylation; Alternative Initiation.
FT	SIGNAL
FT	CHAIN
FT	CHAIN
FT	INIT_MET
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DOMAIN
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	DOMAIN
FT	CARBOHYD
FT	CARBOHYD
QO	SEQUENCE







Mon Nov 5 08:22:43 2001

us-09-006-352-2.rsp



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 31, 2001, 12:38:21 ; Search time 19.71 Seconds  
(without alignments)  
2013.775 Million cell updates/sec

Title: US-09-006-352-2  
1634  
Sequence: 1 MRALEPGSLCLVLAIPA.....RVANMPGLNSVRERPLPVH 300

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP:archaea:\*  
2: SP:bacteria:\*  
3: SP:fungi:\*  
4: SP:human:\*  
5: SP:invertebrate:\*  
6: SP:mammal:\*  
7: SP:mhc:\*  
8: SP:organelle:\*  
9: SP:phage:\*  
10: SP:plant:\*  
11: SP:rodent:\*  
12: SP:unclassified:\*  
13: SP:vertebrate:\*  
14: SP:virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634	100.0	300	4 095407	095407 homo sapien
2	444	27.2	401	4 000300	000300 homo sapien
3	440.5	27.0	372	4 09UH94	09UH94 homo sapien
4	425.5	26.0	401	11 008727	008727 rattus norv
5	424.5	26.0	401	11 008712	008712 mus musculu
6	395	24.2	302	13 09PU50	09PU50 mus musculu
7	340.5	20.8	439	4 016042	016042 homo sapien
8	333.5	20.4	459	11 062327	062327 mus musculu
9	327	20.0	482	11 088734	088734 mus musculu
10	291.5	17.8	655	11 09EP05	09EP05 mus musculu
11	287	17.6	655	11 075509	075509 homo sapien
12	282.5	17.3	348	14 057277	057277 monkeypox v
13	280.5	17.2	348	14 057103	057103 monkeypox v
14	280.5	17.2	348	14 057108	057108 monkeypox v
15	276	16.9	349	14 057100	057100 monkeypox v
16	274	16.8	349	14 057291	057291 monkeypox v
17	274	16.8	349	14 057101	057101 monkeypox v
18	274	16.8	349	14 057102	057102 monkeypox v
19	273	16.7	349	14 057099	057099 monkeypox v

20	265	16.2	350	14 057116	057116 cowpox viru
21	264.5	16.2	355	14 085308	085308 cowpox viru
22	262.5	16.1	349	14 057110	057110 variola vir
23	262.5	16.1	349	14 057111	057111 variola vir
24	262.5	16.1	349	14 089118	089118 variola vir
25	262.5	16.1	349	14 089098	089098 variola vir
26	262	16.0	348	14 057112	057112 variola vir
27	262	16.0	348	14 085407	085407 variola vir
28	261.5	16.0	349	14 057284	057284 camelpox vi
29	261.5	16.0	349	14 057098	057098 camelpox vi
30	259.5	15.9	349	14 057305	057305 cowpox viru
31	259.5	15.9	360	14 057118	057118 cowpox viru
32	258.5	15.8	351	14 057117	057117 cowpox viru
33	258.5	15.8	351	14 073559	073559 cowpox viru
34	257.5	15.8	326	14 057120	057120 cowpox viru
35	257.5	15.8	349	14 057097	057097 camelpox vi
36	254.5	15.6	326	14 057122	057122 cowpox viru
37	254.5	15.6	349	14 057109	057109 variola vir
38	253.5	15.5	347	14 057115	057115 cowpox viru
39	251.5	15.4	347	14 057119	057119 cowpox viru
40	250.5	15.3	351	14 057121	057121 cowpox viru
41	249	15.2	283	6 09XS28	09XS28 cercopithe
42	246	15.1	283	4 092956	092956 homo sapien
43	246	15.1	283	4 09UM65	09UM65 homo sapien
44	245.5	15.0	350	14 057123	057123 cowpox viru
45	239	14.6	616	4 09Y606	09Y606 homo sapien

## ALIGNMENTS

RESULT 1  
095407 PRELIMINARY: PRT: 300 AA.

AC 095407;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE DECOY RECEPTOR 3 (M68) (M68C) (M68B) (DJ583p15.1.1).  
GN DCR3 OR TR6 OR TNFRSF6B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99087326; PubMed=9872321;  
RA Picot R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,  
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,  
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,  
RA Goddard A.D., Bortstein D., Ashkenazi A.;  
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and  
RT colon cancer.";  
RL Nature 396:699-703(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99253915; PubMed=10318773;  
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;  
RT "A newly identified member of tumor necrosis factor receptor  
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";  
RL J. Biol. Chem. 274:13733-13736(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX TISSUE=PANCREAS;  
RX MEDLINE=20126500; PubMed=10655513;  
RA Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V.,  
RA Soderman A., Galloway S.M., Liu O., Austin C.P., Caskey C.T.;  
RT "Overexpression of M68/DCR3 in human gastrointestinal tract tumors  
RT independent of gene amplification and its location in a four-gene  
RT cluster.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).  
RN [4]



RP	SEQUENCE FROM N.A.
RA	Matthews L.:
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF104419; AAD03056.1; -
DR	EMBL; AF134240; AAF28688.1; -
DR	EMBL; AF217796; AAF36244.1; -
DR	EMBL; AF217793; AAF36885.1; -
DR	EMBL; AF217794; AAF36886.1; -
DR	EMBL; AL121845; CAC03668.1; -
DR	HSSP; P25942; ICDF
DR	InterPro; IPR000561; -
DR	InterPro; IPR001368; -
DR	Pfam; PF00020; TNFR_C6; 4.
DR	ProDom; PD000771; -; 1.
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR	PROSITE; PS00505; TNFR_NGFR_2; 2.
KW	Receptor.
SQ	SEQUENCE 300 AA: 32679 MW: F90AE8E3718449AF CRC64;
Query Match	100.0%; Score 1634; DB 4; Length 300;
Best Local Similarity	100.0%; Pred. No. 7.7e-139;
Matches 300:	Conservative 0; Mismatches 0; Indels 0; Gaps
QY	1 MAALGGPSILSLCLVALPALLPVAAGVAVETPPYPVRDAENGEERLYVCACQCPCTVOR 60
Dp	1 MAALGGPSILSLCLVALPALLPVAAGVAVETTPYPRDAEFIERLVCAQCPCPTTVOR 60
OY	61 PCRRSPPTCGPCPRHRYTQFWNTLERRCNYNLCSGEFEFARACHATHNACGRIGFF 120
Dp	61 PCRBDSPPTCGPCPRHRYTQFWNTLERRCNYNLCSGEREEARACHATHNACGRIGTF 120
OY	121 AHAGCCEAHACPGAGAGIATGTSONTQOCPCPGPFISASSSSSECCPHRNCTALGLA 180
Dp	121 AHAGCCEAHACPGACAGIATGTSONTQOCPCPGPFISASSSSSECCPHRNCTALGLA 180
OY	181 LNVSSTSHDPLCHSCGFPFLSTVPNGAECEERAYIDPVAFODISIKRLOPLDALPAPE 240
Dp	181 LNVSSTSHDPLCHSCGFPFLSTVPNGAECEERAYIDPVAFODISIKRLOPLDALPAPE 240
OY	241 GWGTPPRAGRALDLKLRRLTELLGAQDGALLVRLLOALRVAMPGLERSVERELPVH 300
Dp	241 GWGTPPRAGRALDLKLRRLTELLGAQDGALLVRLLOALRVAMPGLERSVERELPVH 300
RESULT	2
0003300	PRELIMINARY; PRT; 401 AA.
ID	000300
AC	000300; 060236;
DT	01-JUL-1997 (TEMBLrel. 04, Created)
DT	01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DE	01-MAR-2001 (TEMBLrel. 16, last annotation update)
DE	OSTEOBROTEGRIN PRECURSOR (OSTEOCALTOGENESIS INHIBITORY FACTOR)
DE	(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11b).
GN	TNFRSF11B OR OCIF OR OCIF.
OS	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBL_TaxId=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	TISSUE=KIDNEY.
RC	MEDLINE=97262071; PubMed=9108485;
RX	Stromer W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA	Stromer W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA	Luetty R., Elliott H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.
RA	DeMarco M., Elliott H.Q., Colombo A., Tan H.-L., Trail G., Sullivan J.
RA	Davy E.M., Bucky N.S., Keshav-Garg L., Hughes T.M., Hill D., Pattison W.
RA	Campbell P., Sander S., Van G., Tarpley J., Detly P., Lee R.,
RA	Sugita S., Boyle W.J.:
RT	Osteoprotegerin: a novel secreted protein involved in the regulation
RL	Cell 89:309-319(1997).

RN	[2]	SEQUENCE FROM N.A.
RC		TISSUE=LUNG FIBROBLAST:
RX		MEDLINE=98151033; PubMed=9492069;
RA		Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA		Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA		Tsuda E., Morinaga T., Higashio K.,
RT		"Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT		osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RL		osteoclastogenesis in vitro."
RL		Endocrinology 139:1329-1337(1998).
RC		SEQUENCE FROM N.A.
RC		TISSUE=PLACENTA:
RX		MEDLINE=98351569; Pubmed=9688283;
RA		Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.,
RT		"Cloning and characterization of the gene encoding human
RT		osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL		Eur. J. Biochem. 254:685-691(1998).
CC	-I-	FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC		OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC		SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC		OSTEOCLASTOGENESIS BY INTERFERING CELL-TO-CELL SIGNALING BETWEEN
CC		STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC	-I-	SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
CC		SMILIARITY).
CC	-I-	SUBCELLULAR LOCATION: EXTRACELLULAR.
CC		TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
CC		KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
CC		A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
CC		THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
CC	-I-	SMILIARITY: CONTAINS A LA-MGF/TNFR-TYPE CYSTEINE-RICH REGION.
DR	EMBL	AB002146; BA25910.1; "
DR	EMBL	AB008832; BA32076.1; "
DR	EMBL	AB008821; BA32076.1; JOINED.
DR	HSSB	U94332; BAB5709.1; "
DR	HSSB	P25942; ICDP.
DR	MM	602643; "
DR	InterPro	IPR000488; "
DR	InterPro	IPR01368; "
DR	Plan	PF00020; TNFR_cf; 3.
DR	PRODOM	PD000771; "- 1.
DR	PROSITE	PS00652; TNFR_NFGR_1; UNKNOWN_1.
DR	PROSITE	PS50050; TNFR_NFGR_2; 2.
DR	SMART	SM00005; DEATH_1.
KW		Glycoprotein; Repeat; cytokine; signal.
FT	SIGNAL	1..21 BY SIMILARITY.
FT	CHAIN	22..401 OSTEOPROTEGERIN.
FT	DOMAIN	23..183 4 X TNFR-CYS.
FT	REPEAT	23..63 TNFR-CYS 1.
FT	REPEAT	64..106 TNFR-CYS 2.
FT	REPEAT	107..143 TNFR-CYS 3.
FT	REPEAT	144..201 TNFR-CYS 4.
FT	DOMAIN	306..365 DEATH DOMAIN.
FT	DISULFID	41..54 BY SIMILARITY.
FT	DISULFID	44..62 BY SIMILARITY.
FT	DISULFID	65..80 BY SIMILARITY.
FT	DISULFID	83..97 BY SIMILARITY.
FT	DISULFID	87..105 BY SIMILARITY.
FT	DISULFID	118..142 BY SIMILARITY.
FT	DISULFID	145..160 BY SIMILARITY.
FT	CARBOHYD	98..98 N-LINKED (GLCNAC. .)
FT	CARBOHYD	132..132 (POTENTIAL).)
FT	CARBOHYD	152..152 N-LINKED (GLCNAC. .)
FT	CARBOHYD	165..165 N-LINKED (GLCNAC. .)
FT	CARBOHYD	178..178 N-LINKED (GLCNAC. .)
FT	CARBOHYD	289..289 N-LINKED (GLCNAC. .)
FT	CONFLICT	263..263 (POTENTIAL).)
QO	SEQUENCE	401 AA; 45996 MW; EB42FA51C9D7C7E CRC64; A -> D (IN REF. 2 AND 3);

Query Match	27.28;	Score 444;	DB 4;	Length 401;
Best Local Similarity	39.68;	Pred. No. 5.4e-32;		
Matches	84;	Conservative	32;	Mismatches 86;
			Indels	10;
			Gaps	4;



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QY 11 LCLVLAALPAPVAVKGAET--PTYMRDAETGERLVCAACPPGTFVQRCRDSPT 68
DB 4 LLLCAL---VFLDISIKMTQETFPFKYLYHDETSKQCLCDKCPGTYLKQCTAKMKP 60
QY 69 TCGPCPRHYTQPMWNLRCRYCNVLCGEREEARACHATHNACRCRTGFFAHAGCLE 128
DB 61 VCAPCPDHYTTSWMTSDCLCSPYCKQYVYKQECNRTNHNVCCKEKGYLEIEFCLK 120
QY 129 HASCPCGAVIAPGPSQNTQOCPCPGTFPSASSSSSEOCQPRNCTALGLALNPGSSS 188
DB 121 HNSCPGFGVQAGTERKNTVCRCRCDGFFSNSTSSKAPCRKHTNCSVGLLLTQKGNAT 180
QY 189 HDLTCTSGTGFPLSTRVPAEE--CERAVIDF 218
DB 181 HDNI---CSGNSESTQKCGIDVTLCEAFRRF 209

RESULT 3
QY 090HP4 PRELIMINARY; PRT; 372 AA.
AC 090HP4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN 11)
RP SEQUENCE FROM N.A.
RA TISSUE=PLACENTA;
RC He 2, -Y, Yang G, -Z, Zhang W, -J, Wu X, -F;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL; AF134187; AAF20168.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
FT NON_TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;
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Query Match 27.0%; Score 440.5; DB 4; Length 372;
Best Local Similarity 41.2%; Pred. No. 1e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;
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QY 34 PTPYMRDAETGERLVCAACPPGTFVQRCRDSPTGCPRRHYTQPMWNLRCRYCNV 93
DB 5 PLYLHDETSKQCLCDKCPGTYLKQCTAKMKTYCACPDHYTDSMTSDECLYCSP 64
QY 94 LCGEREERARACHATHNACRCRTGFFAHAGCLEHASCPCGAVIAPGPSQNTQOCPC 153
DB 65 VCKELQYVAGQECNRHTNVCCKEKGYLEIEFCLKHRSRCPGFGVQAGTERKNTVCRCR 124
QY 154 PCTGTSASSSSSEOCQPRNCTALGLALNPGSSSHDTLCTSGTGFPLSTRVPAEE--C 211
DB 125 PDGFFSNSTSSKAPCRKHTNCSVGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTL 181
QY 212 ERAVIDF 218
DB 182 EEAFRRF 188

RESULT 4
QY 008727 PRELIMINARY; PRT; 401 AA.
AC 008727;
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DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF).
GN TNFRSF11B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN 11)
RP SEQUENCE FROM N.A.
RA TISSUE=INTESTINE;
RC MEDLINE-97262071; PubMed-9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luehly R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density";
RL Cell 89:309-319(1997).
CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; U94330; AAB53707.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1
FT CHAIN 21
FT DOMAIN 22 401
FT REPEAT 23 201
FT REPEAT 23 63
FT REPEAT 64 106
FT REPEAT 107 143
FT REPEAT 144 201
FT REPEAT 201 365
FT DOMAIN 365
FT DISULFID 41
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 97 105
FT DISULFID 105 142
FT DISULFID 142 160
FT CARBOHYD 145 160
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
SQ SEQUENCE 401 AA; 46192 MW; FEC6A31FD4E573A CRC64;
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Query Match 26.0%; Score 425.5; DB 11; Length 401;
Best Local Similarity 39.5%; Pred. No. 2.5e-30;
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;
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QY 34 PTPYMRDAETGERLVCAACPPGTFVQRCRDSPTGCPRRHYTQPMWNLRCRYCNV 93
DB 26 PLYLHDETSKQCLCDKCPGTYLKQCTAKMKTYCACPDHYTDSMTSDECLYCSP 85
QY 94 LCGEREERARACHATHNACRCRTGFFAHAGCLEHASCPCGAVIAPGPSQNTQOCPC 153
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DB 86 VCKELQTVKOEBCNRTNHYVCECEBGRVLELBECLKHKRSCPGVLQAGFPERNTVCKRC 145
OY 154 PGTFSASSSSSEOCOPHRNCTALGLALNVPGSSHDLTCTGTFPLSTRVPAEE--C 211
DB 146 PDGFSGSGSSKAPCRKHTNCSLCLLLOKGNATHDNV---CSGNREATONCGIDVTLG 202
OY 212 ERAVIDFAFODISIKRLOLQAL 236
DB 203 EEAFFRAVPTKIIPMWLSVLDL 227

RESULT 5
O08712 PRELIMINARY: PRT: 401 AA.
AC 008712.070202.
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF).
GN TNSRFL1B OR OPG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-KIDNEY;
RA MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Desose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Geeg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RT Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-129/OLA, AND NIH SWISS.
RA MEDLINE=96382527; PubMed=9714633.
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA Higashio K.;
RA "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
CC - FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC - SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
CC - TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
CC PLACENTA. NOT DETECTED IN SPLEEN.
CC - DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
CC 15 TO DAY 17.
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: U94331. AAB53708.1.
DR EMBL: AB013698. BAA38260.1.
DR EMBL: AB013903. BAA33368.1.
DR EMBL: AB013899. BAA33368.1. JOINED.
DR EMBL: AB013900. BAA33368.1. JOINED.
DR EMBL: AB013901. BAA33368.1. JOINED.
DR EMBL: AB013902. BAA33368.1. JOINED.
DR HSSP: P25942. ICDF.
DR GSSP: MG1:109587. TnfRsf11b.
DR InterPro: IPR000488.
DR InterPro: IPR001368.
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DR Pfam: PF00020; TNFR_C6; 3.
DR ProDom: PD000771; -. 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR SMART: SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401 OSTEOPROTEGERIN.
FT DOMAIN 23 201 4 X TNFR-CYS.
FT REPEAT 23 63
FT REPEAT 64 106 TNFR-CYS 1.
FT REPEAT 107 143 TNFR-CYS 2.
FT REPEAT 144 201 TNFR-CYS 3.
FT REPEAT 201 365 TNFR-CYS 4.
FT DOMAIN 365 401 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 289 289 R -> P (IN STRAINS 129/OLA AND NIH
FT VARIANT 138 138 SWISS).
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH
FT VARIANT 161 161 SWISS).
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH
FT VARIANT 296 296 SWISS).
SQ SHOUENCE 401 AA; 45923 MW; CAA6102DB312470 CRC64.

Query Match 26.08; Score 424.5; DB 11; Length 401;
Best Local Similarity 39.08; Pred. No. 3; le-30;
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;

OY 34 PTPYPMWDAETGERLVCAOCPPGTGVORPCRPDSPTTQCPGPPRHVYQFVNYLERCRVCNV 93
DB 26 PKLYHYDPETGHOLDCDKCAPGYTLKQHCYVTKTLQVCPDHSYDLSWHTSDECVYCS 85
OY 94 LCGEREERARACHATNHRACRCRGTGFPAHAGFCLHASCPCPGAGVAPQTPSQNTQOCOPC 153
DB 86 VCKELQTVKOEBCNRTNHYVCECEBGRVLELBECLKHKRSCPGSVVQACTPERRNTVCKKC 145
OY 154 PGTFSASSSSSEOCOPHRNCTALGLALNVPGSSHDLTCTGTFPLSTRVPAEE--C 211
DB 146 PDGFSGSGSSKAPCRKHTNCSLCLLLOKGNATHDNV---CSGNREATONCGIDVTLG 202
OY 212 ERAVIDFAFODISIKRLOLQAL 236
DB 203 EEAFFRAVPTKIIPMWLSVLDL 227

RESULT 6
O09P050 PRELIMINARY: PRT: 302 AA.
AC O09P050.
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE DECOY RECEPTOR.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei;
OC Protactinopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
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RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor receptor homolog is up-regulated in the brook
RL trout (Salvelinus fontinalis) ovary at the completion of ovulation.";
EMBL: AF156738; AAD56428.1; -.
DR HSSP: P19438; 1EXT.
DR InterPro: IPR000561; -.
DR pfam: PF00020; TNFR.c6; 4.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR SMART: SM00208; TNFR; 1.
KW Receptor.
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 24.2%; Score 395; DB 13; Length 302;
Best Local Similarity 34.3%; Pred. No. 1e-27;
Matches 82; Conservative 44; Mismatches 101; Indels 12; Gaps 7;

QY 35 TYPWRATGGERLYVCAQCPPTGFVQRCRDSPTTCGCPPTPHYTQPMWYLERCRICNL 94
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 22 TKNDRDYRGLSTVCDRCPTGYTLRAPCSAMRKSDCAECNGAVTEPMWHSKCLRCS-M 80
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
QY 95 CGREEEARACHATNRACRRTGFEAHAGF--CLEHASCPPGAGVIAPGTPSONTOCQP 152
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 81 CAENOVVQKCEFSNNCECECKGYFNKKYEACIKHKECPGYGANTGTTPHODECYO 140
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
QY 153 CPGPTFSASSSSSECCOPHRNCTALGLALNVPGSSSHDTLCTSCGTPPLSTRVGAEECE 212
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 141 CQAGFSEVSSAAKATGLSNCKVGLRVYLKQDMHNTLCASC--YDLKTR-DGAEYLH 197
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
QY 213 RAVIDVY--AFQDISIKRLQRLQALPAPEGMGPTPRAGALQLKLRRLTELLCAOD 269
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 198 EILPFPFIQLHQTMGIKRMKRL--AMRLQPEGGCKPLIG--AVMKRNRLGHDHFNMSWD 252
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :

RESULT 7
Q16042 PRELIMINARY; PRT; 439 AA.
AC Q16042;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Genz R.,
RA Brochhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytochrome 2;231-237(1990).
EMBL: S63368; AAB19824.1; -.
DR HSSP: P25942; 1CDF.
DR InterPro: IPR001368; -.
DR pfam: PF00020; TNFR.c6; 4.
DR PRODOM: PD000771; -.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
DR SMART: SM00208; TNFR; 2.
SQ SEQUENCE 439 AA; 46090 MW; FEBCBE329CC67FE6 CRC64;

Query Match 20.8%; Score 340.5; DB 4; Length 439;
Best Local Similarity 29.7%; Pred. No. 1.1e-22;

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Matches 89; Conservative 43; Mismatches 115; Indels 53; Gaps 11;

QY 30 VAEPTPYPMWDAETGE-----RLVCAQCPPTGFVQRCRDSPTTCGCPPTPH 77
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DB 5 VAEPTPYAP-----EPGSTCRRLREYDDQTQWCKSCSKSPGAKAFCKRTSDTVDSCEDS 60
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
QY 78 YVQFMWYLERCRYCNVLGGEREEARACHATNRACRRTGFEAHAGF-----FCLHAS 131
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 61 YQLMMWVPECLSCGSRSSDQVETQACTREQNRICTCRPGWYCALSKQEGCHLAPLRK 120
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
QY 132 CPGGAGVIAPGTPSONTOCQCPPTFSASSSSSECCOPHRNCTALGLALNVPGSSSHDT 191
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 121 CRPGFGARPGTSDVYCKPCAPGTFSSNTSTSDICRPHQICNVVA---IFGNASMDA 176
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
QY 192 LCTSCGTGFLSTRVPGAEECEARAVIDVFAQDISIKRLQRLQALPAPE-----GNGPTP 246
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 177 VCRSTS--PRSNAPGAVHLPPV-----STRSQHTQTPPTPSTAPSTFLPMPGSP 227
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
QY 247 RA-----GRAALQLKLRRLTELLGAODGALLVRLQAL--RVARNP-GLERSVREPLP 298
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 228 PARGSTGDFALPVGLIVGYTAL-----GLLIIGVNCVIMTQVKKRPDLQREAKVPHLP 282
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :

RESULT 8
Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95178448; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5;726-727(1994).
EMBL: X76401; CAA53981.1; -.
DR HSSP: P19438; 1NCF.
DR InterPro: IPR001368; -.
DR pfam: PF00020; TNFR.c6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
DR SMART: SM00208; TNFR; 1.
FT NON_TER 1
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 20.4%; Score 333.5; DB 11; Length 459;
Best Local Similarity 29.7%; Pred. No. 5.1e-22;
Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;

QY 46 RLVCACCPPTGFVQRCRDSPTTCGCPPTPHYTQPMWYLERCRYCNVLGGEREEARAC 105
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DB 37 QMCCARCPGQYVKKHPCNKSDTVACDCASMYTVVWNOEFTRLSCSSSSCTDQVETFRAC 96
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
QY 106 HATHNRACRRTGFE-----AHAGF--CLEHASCPPGAGVIAPGTPSONTOCQCPPTGF 158
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 97 TKQGNVYCACENGRYCALKTHSSGCRQCMRLSKGPGFVASSRANGVNLCKACAPGTF 156
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
QY 159 SASSSSECCOPHRNCTALGLALNVPGSSSHDTLCT---SCTGFLSTRVPGAEECEERA 214
   1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :

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DB 157 SDTSTSDVCRPHRICSTLA-----IPGNASPDVACAPESPTLSAIPRTLVVSQPEPTRSQ 212  
 OY 215 VIDFVAFODISIKRLQRLQALAEPEGWPTP-----RAGRAALQKLRRLTELLGAOD 269  
 DB 213 PLD-----QEPGSGTSPISITLSL-----GSTPIIEOSTKSGISLPIGLIVGTVSL----- 257  
 OY 270 GALVRLQAL-----RVANMPLEKSVREERFLP 298  
 DB 258 GLMLGLVNCFLVQKRRKPSCLQDAVPIHP 290

RESULT 9  
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 ID 088734 PRELIMINARY: PRT: 482 AA.  
 AC 088734;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE P80 TNF-ALPHA RECEPTOR.  
 GN TNFR2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huile B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;  
 RT "The Mouse Tumor Necrosis Factor Receptor Gene: Genomic Structure and  
 RT Characterization of the two Transcripts."  
 RL Genomics 0:0-0(0).  
 DR EMBL: Y14619; CAI:74969.1; JOINED.  
 DR EMBL: Y14621; CAI:74969.1; JOINED.  
 DR EMBL: Y14621; CAI:74969.1; JOINED.  
 DR EMBL: Y14622; CAI:74969.1; JOINED.  
 DR EMBL: Y14623; CAI:74969.1; JOINED.  
 DR EMBL: Y14679; CAI:74969.1; JOINED.  
 DR HSSP: p19438; INCE.  
 DR InterPro: IPR001368;  
 DR Pfam: PF00020; TNFR\_C6; 4.  
 DR ProDom: PD000771;  
 DR PROSITE: PS00652; TNFR\_LGFR\_1; 2.  
 DR PROSITE: PS00650; TNFR\_LGFR\_2; 3.  
 DR SMART: SM00208; TNFR; 1.  
 SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 20.0%; Score 327; DB 11; Length 482;  
 Best Local Similarity 29.3%; Pred. No. 2e-21;  
 Matches 82; Conservative 43; Mismatches 109; Indels 46; Gaps 10;  
 OY 46 RLVCACCPGPTGVORPCRR-----DSPTTCGCPGPRHYQFNNYLERGRCYNVLCGER 98  
 DB 52 QMKCAKCPGQYVHKHCNKTSDTVACADSDTVACADCEAMTYQVNNORFTLCSSSSCSTD 111  
 OY 99 EEEAACHATYHARACRTGFP-----AHAGF---CLEHASCPPGAGYIACPTSONOQO 151  
 DB 112 QVETRACTGQORVACAGARCAKLTGSGSCROCMRLSKGPGFVASSAPANGVLCK 171  
 OY 152 PPPGFFSSSSSSSBOCPHRCALGALNVSSSHDCTCT-----SCGFPSTSTVPG 207  
 DB 172 ACAPGFSPTSTSDVCRPHRICSTLA-----IPGNASPDVACAPESPTLSAIPRTLVVSQ 227  
 OY 208 AECECAVYDFAFODISIKRLQRLQALAEPEGWPTP-----RAGRAALQKLRRLT 262  
 DB 228 PEPTSPD-----QEPGSGTSPISITLSL-----GSTPIIEOSTKSGISLPIGLIVGTV 277  
 OY 263 ELGAGDQALVRLQAL-----RVANMPLEKSVREERFLP 298  
 DB 278 SL-----GLMLGLVNCFLVQKRRKPSCLQDAVPIHP 312

RESULT 10  
 Q9EPUS

ID Q9EPUS PRELIMINARY: PRT: 655 AA.  
 AC Q9EPUS;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE DR6  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=KIDNEY;  
 RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,  
 RA Minami M.;  
 RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6  
 RT (DR6)."  
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AF322069; AAC38115.1;  
 DR EMBL: AF322069; AAC38115.1;  
 SQ SEQUENCE 655 AA; 71909 MW; 1A97C1A32799E4FB CRC64;

Query Match 17.8%; Score 291.5; DB 11; Length 655;  
 Best Local Similarity 28.6%; Pred. No. 4.2e-18;  
 Matches 73; Conservative 37; Mismatches 130; Indels 15; Gaps 3;  
 OY 12 LCLVLAFLPVPVAVRGAETPTYPWRDAETGERLVCACCPGPTGVORPCRRDSTPTCG 71  
 DB 30 LLLIGFLSTIAOPEQKTLSPGTYRHVDRTGTGVLCDKCPAGTVSEHCTNMSLRVCS 89  
 OY 72 PCPPRHQYQFNNYLERGRCYNVLCGEREERACHATHNACRCRGPFAHAGFLEHAS 131  
 DB 90 SCPATFTRIHNGIERCHDCSQPCPMIRLCAALTDCECCPCPPGQMSNGTCAPIHV 149  
 OY 132 CPBGAGYIACPTSONOQOCCPPTGTSASSSSBOCPHRCALGALNVSSSHHT 191  
 DB 150 CPVGVKRRKGTENDVACKANGTSDVSSVMKKAHTDCLQNLVYKGTETDN 209  
 OY 192 ICTSGTGPLL---STRVGAECERAVYDFAFODISIKRLQRLQALAEPEGWPTPRA 248  
 DB 210 VC-----GMRLEFSSSTNPSSGTVTFSHPHEMSHDVPSSTYE-----PGMNSTDSN 257  
 OY 249 GRALQKLRRLTE 263  
 DB 258 STASVTRKVPGIEE 272

RESULT 11  
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 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
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 GN DR6 OR DJ181J13.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G.,  
 RA Vincent C., Aggarwal B.B., Dixit V.M.;  
 RT Identification and functional characterization of DR6, a novel death  
 RT domain-containing TNF receptor.  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Parker A.;  
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF068868; AAC34583.1;







Mon Nov 5 08:22:44 2001

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Page 8

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RN [1]
RP SPOUNCE FROM N.A.
RC STRAIN=FAIRE-1970 (CONGO-8);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted Feb-1997 to the EMBL/GenBank/DBJ databases.
DR EMBL: 088842; AAB94367.1; -.
DR HSSP: p25942; ICDF.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNER_C6; 2.
DR ProDom: PD000771; -.
DR PROSITE: PS00652; TNER_NGFR_1; 2.
DR PROSITE: PS00500; TNER_NGFR_2; 2.
DR SMART: SM00208; TNER; 1.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;
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OY 9 LSLACLVLALPALPVPVAVGVAETPTYPVDAETGERLVCAQCPPTGVQRPCRRDSPT 68
DB 10 LFLSCILLNGRIAPHAPSNGKCKDNEYRSRN-----LCCLSCPPGTYYASRLCDSKNT 63
OY 69 TCGPCPPRIHYTOFMNYLERCRYCNVLCGEREEERACRCHATHNRCRCRTGFF-----AH 122
DB 64 OCTPGSGDFTFTSHNNHLDACLSCNGRCDNSQVETRSCNTNHNRLCECSPGYCYLLKGSSG 123
OY 123 AGFCLEHASCPPGAGVIAAGTPSQNTQCQPCPPGTFSASSSSSSBOCPHRCCTALGLAN 182
DB 124 CRTCLSKTKRCIGYGV-SGYTSDGVICSPCGGTYSHTVSSIDKCEPVTSNTFNVIDE 182
OY 183 VPGSSSHDTLCTSCGFPPLSTRVPAE 209
DB 183 INIPVNDISCTRTTTGLSISISTSE 209
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DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID-10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIGERIA-1971 (71-0082);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: 087844; AAB94361.1; -.
DR HSSP: p25942; ICDF.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNER_C6; 2.
DR ProDom: PD000771; -.
DR PROSITE: PS00652; TNER_NGFR_1; 2.
DR PROSITE: PS00500; TNER_NGFR_2; 2.
DR SMART: SM00208; TNER; 1.
SQ SEQUENCE 349 AA; 38239 MW; DFC6C280D478F2422 CRC64;
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DB 10 LFLSCILLNGRIAPHAPSNGKCKDNEYRSRN-----LCCLSCPPGTYYASRLCDSKNT 63
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OY 69 TCGPCPPRIHYTOFMNYLERCRYCNVLCGEREEERACRCHATHNRCRCRTGFF-----AH 122
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OY 123 AGFCLEHASCPPGAGVIAAGTPSQNTQCQPCPPGTFSASSSSSSBOCPHRCCTALGL 179
DB 124 CRTCLSKTKRCIGYGV-SGYTSDGVICSPCGGTYSHTVSSIDKCEPVTSNTFNVIDE 182
OY 180 ALNVPSSSHDTLCTSCGFPPLSTRVPAE 209
DB 183 EIML--YPVNDISCTRTTTGLSISISTSE 210
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 617)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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DNA Sequencing by: Incyte Genomics, Inc.
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98 gGluGlnGlnAlaArgAlaCysAlaThrHisAsnArgAlaCysArgC 115
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115 ysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnHisAlaSer 131
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248 aglyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeu 265

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REFERENCE 1 (bases 1 to 679)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9677 row: h column: 21
High quality sequence stop: 672.
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NciI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 113 a 239 c 204 g 123 t
ORIGIN
alignment_scores:
Quality: 1020.00 Length: 192
Ratio: 5.312 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-006-352-2 x BE878006 ..
Align seg 1/1 to: BE878006 from: 1 to: 679
109 HisAsnArgAlaCysArgCysArgThrglyphepheAlaHisAlaGlyph 125
|||||
12 CACACACCGTCTCGCTCGCCACCGGCTTCTTCGGCAGCGCTGGTTT 61
125 ecysleuglnHisAlaSerCysProProGlyAlaGlyValIleAlaProG 142
|||||
62 CTGCTTGGAGCAGCAGTCGTCACCTGGTGGCGGCTGATTGCCCGG 111
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142 lYthrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPhe 158
|||||
112 GCACCCCGACGACAGACACGACATGTCAGCGCTTCCATCAGACCTTC 161
159 SerAlaSerSerSerSerSerGlnCysGlnProHisArgAsnCysTh 175
|||||
132 TCAGCAGCAGCTCCAGCTCAGAGCAGTGCAGCCGCCACCCAACTGCAC 211
175 rAlaleuglnLeuAlaleuAsnValProGlySerSerSerHisAspThr 192
|||||
212 GGCCCTGGGCGCTGGCCCTCATGTGTCAGGCTCTTCCATCAGACCC 261
192 euCysThrSerCysThrGlypheProLeuSerThrArgValProGlyAla 208
|||||
262 TGTCACACAGCTGCACCTGCTTCCCTCCACACAGAGGTACAGAGACT 311
209 GlnGlnCysGlnArgAlaValIleAspPheValAlaPheGlnAspIleSe 225
|||||
312 GAGGAGTGTAGCGTGGCTGATCGACTTGTGTGCTTCCAGGACATCTC 361
225 rIleLysArgLeuGlnArgLeuLeuGlnAlaleuGlnAlaProGlnGlyT 242
|||||
362 CATCAAGAGCTGCAGCGCTGCTGCAGGCTCGAGGCGCCGAGGCGCT 411
242 rpglyProThrProArgAlaGlyArgAlaAlaleuGlnLeuLysLeuArg 258
|||||
412 GGGCTCCACACCAAGAGGCGGCGCGCGCTTGCACCTGACCTGAGTGGT 461
259 ArgArgLeuThrGlnLeuLeuGlnAlaGlnAspGlyAlaLeuLeuValAr 275
|||||
462 CGGGGCTCAGCAGGACTCTGGGGCGCAGAGCGGGGCTGTGTGTGCG 511
275 gLeuGlnGlnAlaleuArgValAlaArgMetProGlyLeuGlnArgSerV 292
|||||
512 GCTGCTGACAGCGCTGCCGCTGCCAGGATGCCGCGCTGAGCGGAGCG 561
292 aArgGlnArgPheLeuProValHis 300
|||||
562 TCCGTGACGCTTCTCCTCGTGGCAC 587
seq_name: gb_est47:AM464298
seq_documentation_block:
LOCUS AM464298 554 bp mRNA EST 24-FEB-2000
DEFINITION BP230015A20G11 Soares normalized bovine placenta Bos taurus cDNA
clone BP230015A20G11 5', mRNA sequence.
ACCESSION AM464298
VERSION AM464298.1 GI:7034466
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 554)
AUTHORS Lewin,H.A., Soares,M.B., Rebeliz,M., Pardinas,J., Liu,L. and Larson
,J.H.
TITLES Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimml 9:
Cross_match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
```







```
229 CAGTGGCCCCAGGACCTTTGTGACGGCGG.TGCCGCCAGACAGCCC 277
67 oThrThcCysGlyProCysProPArgHisTyrThcGlnPheTrpAsn 84
|||||
278 CAGACAGTGTGGCCGTGTCCAGCGGCACCTACACGAGTCTGGAACT 327
84 yTLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGlu 100
|||||
328 ACCGTGGAGCGCTGCTACTGCAACGCTCTCGGGGAGCGTAGAGAG 377
101 GluAlaArgAlaCysHisAlaThcHisAsnArgAlaCys...ArgCysArg 116
|||||
378 GAGCAGCGGCTGCTCCAGCCACCC.....AAACCGTGCCTGCCGTGCG 421
116 gThcGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysP 133
|||||
422 CACCGGCTTCTTCGCGCAGCGTGTCTGCTTGAGAGCAGCATCGTTC 471
133 rOPrOGlyAlaGlyValIleAlaPArgGlyThrProSerGlnAsnThrGln 149
|||||
472 CACCTGGTGGCGGCGTATTGCCCGGGGACCCCGAGCAGAACACGCGAG 521
150 CysGlnProCysProPArgGlyThrPheSerAlaSerSerSerSerG 166
|||||
522 TGCCAGCGGCTGCCCGCAGGACCTTCTCAGCGCAGCAGCTCAGCTCAA 571
166 uGlnCysGlnPProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsn 183
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572 GCACTGGCAGNCC.CACCGGAATGCACGGCCT...GGGCTTGCCCTCAATG 617
183 aPArgGly 185
|||||
618 TGCCAGGT 625
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seq\_name: gb\_est42:AW083241

seq\_documentation\_block:

LOCUS AW083241 692 bp mRNA EST 14-OCT-1999  
DEFINITION xc07a04.x1 NCI-CGAP Co21 Homo sapiens cDNA clone IMAGE:2583534 3'  
similar to TR:095407 095407 DECOY RECEPTOR 3.; contains 1L.b1 MER22  
repetitive element.; mRNA sequence.

ACCESSION AW083241  
VERSION AW083241.1 GI:6038393

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 692)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 414.

Location/Qualifiers

1..692

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2583534"

/clone\_lib="NCI-CGAP\_CO21"

/tissue\_type="moderately differentiated adenocarcinoma"

/lab\_host="DH10B"

/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Normalized to cot >500. Average insert size 1.04kb.  
by Life Technologies."

BASE COUNT 136 a 205 c 235 g 115 t 1 others

alignment\_scores:

Quality: 865.50 Length: 199  
Ratio: 4.678 Gaps: 2  
Percent Similarity: 92.965 Percent Identity: 88.945

alignment\_block:

us-09-006-352-2 x AW083241/rev

Align seg 1/1 to reverse of: AW083241 from: 1 to: 692

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103 ArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPh 119
|||||
689 CGGTCCGCGAGCGCTTCCAGCAGCAGCAGCAGCTGCTCCATCGCGCAGGTT 640
119 ePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysProArgGlyA 136
|||||
639 TTTTGGCAGCGCTG...TTTCTGTGAGCAGCAGCATCGTCCACCTGT.G 594
136 IAGlyValIleAlaPArgGlyThrProSerGlnAsnThrGlnCysGlnPro 152
|||||
593 CCGGCGTATTGCCCGGGGACCCCGAGTCCAGAACACCCAGCTGCCAGCGG 544
153 CysProPArgGlyThrPheSerAlaSerSerSerSerSerGlnCysG 169
|||||
543 TGCCCCCAGGACCTTCTCAGCAGCAGCAGCTCAGCTAGAGCACTGCCA 494
169 nProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGly 186
|||||
493 GCCCAGCGCAACTGCACGCGGCTGGCGCTGCCCTCAATGTGCAGAGCT 444
186 eSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSer 202
|||||
443 CTCTCTCCAGTACACCTGTGCACAGCTGCTGCTGCTGCTGCTGCTGCTG 394
203 ThrArgValProGlyAlaGluGluCysGluArgAlaValIleAspPhe 219
|||||
393 ACCAGGATACAGGACGTGAGAGAGTGTAGCGTCCGCTCATCGACTTTGT 344
219 IAlaPheGlnAspIleSerIleLysArgLeuGlnArgLeuGlnAlaL 236
|||||
343 GCGTTTCCAGGACATCTCCATCAGAGAGCTGACGCGCTGCTGCAGAGGCC 294
236 eUGluAlaProGluGlyTyrPglYProThrProAlaGlyAlaArgAla 252
|||||
293 TCGAGGCGCCCGAGGCGTGGGCTCCGACACAGGCGCGCGCGCGGCC 244
253 LeuAlnLeuLys.LeuArgArgArgLeuThrGluLeuLeuGlyAlaGln 269
|||||
243 TTGCAGCTGAAACTTGGCTCGCGGCTACGAGAGCTCTGGGGGCGCAGG 194
269 sPGlyAlaLeuValArgLeuGlnAlaLeuArgValAlaArgMet 285
|||||
193 ACGGGGCGCTCTGTGGCGCTGCTGCAGGCGCTGCGCGCGCGCAGGATG 144
286 ProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 300
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143 CCCGCGCTGCAGCGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 99
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seq\_name: gb\_est44:AW262121

seq\_documentation\_block:

LOCUS AW262121 600 bp mRNA EST 28-DEC-1999  
DEFINITION xg31d04.x1 NCI-CGAP Lu28 Homo sapiens cDNA clone IMAGE:2752231 3'  
similar to TR:095407 095407 DECOY RECEPTOR 3.; contains TARI.b1











Mon Nov 5 08:22:44 2001

us-09-006-352-2.1st

Page 8

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VERSION      AM662363.1  GI:7454901
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS      1 (bases 1 to 514)
TITLE        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT      Tumor Gene Index
              Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgap@remail.nih.gov
              Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
              Emmert-Buck, M.D., Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Greg Lennon, Ph.D.
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              image.llnl.gov/image/html/resources.shtml
              Seq primer: -400P from Gibco
              High quality sequence stop: 368.
              Location/Qualifiers
                1..514
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_1lb="NCI:CGAP Col4"
                /tissue_type="moderately-differentiated adenocarcinoma"
                /lab_host="DH10B"
                /note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; Salt:
                Site: 2; Notti: Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.7 kb. Life Technologies catalog #:
                11531-019"
BASE COUNT   113 a 156 c 159 g 85 t 1 others
ORIGIN
alignment_scores:
  Quality: 653.00      Length: 131
  Ratio: 5.102         Gaps: 0
  Percent Similarity: 97.710  Percent Identity: 97.710
alignment_block:
US-09-006-352-2 x AM662363/rev ..
Align seg 1/1 to reverse of: AM662363 from: 1 to: 514
170 ProHISARGASnCYsThralaleuG1yleuAlaleuasnValProGlyse 186
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
514 CCCACAGCAACTGCACGGCTGGGGCTGGCCCTCAATGTGCAGAGGCTC 465
186 rISetSerHISAspThrleuCYsThrsrCYsThnglypHeProleuSert 203
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
464 TTCTCCCATGTACACNCTGTCACACGCTGCTGCTCCCTCCAGCA 415
203 hArGyAlaProGlyAlaGluLucySGluArGAlaValIleAspHeVal 219
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
414 CCAGGCTACAGAGACTGAGAGTGTGACGTCGCGCACGACCTTTGG 365
220 AlaPheGlnAspIleSerIleleuArGleuGlnArGleuGlnAlaLe 236
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
364 GCTTTCAGGACATCTCATCAAGAGGCTGACAGGCTGCTGAGGCTCT 315
236 uGuaIAProGluGlyTrpGlyProTrnProArGAlaGlyArGAlaAla 253
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
314 CGAGGCGCCGAGGCGCTGGGCTCGAGACCAAGGCGGCGCGCGGCT 265
253 euGlnleuAspLeuArGArGleuThrGluLeuGluGlyAlaGlnAsp 269
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
264 TGAAGTGAAGCTGCGTGGCGGCTCAAGAGGCTCCGCGGCGGCGAGAC 215
```

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270 G1yAlaLeuLeuValArGleuGlnAlaLeuArGAlaAlaArGmetPr 286
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
214 GGGCGCTGCTGTGCTGCGCTGTCAGAGCGCTGGCCGTCAGAGATGCC 165
286 oGlyLeuGlnArGSerValArGAlaArGpHeleuProValHis 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
164 CGGCTGAGACGAGCGCTCCGACGCTTCTCTCTCTCTGAC 122
seq_name: gb_est24:AI718743
seq_documentation_block:
LOCUS      AI718743      475 bp      mRNA      EST      10-JUN-1999
DEFINITION as55h04.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2353399.3, mRNA sequence.
ACCESSION  AI718743
VERSION    AI718743.1  GI:5035999
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS    1 (bases 1 to 475)
            Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacey,M., Le,N., Lennon,G., Merrin,M., Martin
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
            WashU-NCI human EST project
            Unpublished (1997)
            Contact: Wilson, R.
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -400P from Gibco
            High quality sequence stop: 467.
            Location/Qualifiers
              1..475
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone_1lb="Barstead aorta HPLRB6"
              /sex="male"
              /dev_stage="adult, age 64"
              /lab_host="DH10B (phage resistant)"
              /note="Organ: aorta; Vector: pTZ19-Pac (Pharmacia) with a
              modified polylinker; Site: 1; EcoRI; Site: 2; Notti: 1st
              strand cDNA was primed with a Not I - oligo(dT) primer [5'
              TGTACGATCGAATGAGGAGGAGCGGCGGCTTTTCTTTTCTTTTCTTTTCTTTT
              3']; double-stranded cDNA was ligated to Eco RI adaptors
              [5' AATTGGATCGAC 3' and 5' GTTGAATCG 3'], digested
              with NotI and cloned into the Not I and Eco RI sites of
              the modified pTZ19 vector. Library constructed by Bob
              Barstead."
BASE COUNT   98 a 153 c 151 g 73 t
ORIGIN
alignment_scores:
  Quality: 644.00      Length: 127
  Ratio: 5.071         Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000
alignment_block:
US-09-006-352-2 x AI718743/rev ..
Align seg 1/1 to reverse of: AI718743 from: 1 to: 475
174 CysThralaleuGlyleuAlaleuasnValProGlySerSerHis 190
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
473 TGCAGGCGCTGGGCTGGCCCTCAATGTGCAGAGCTTCTCTCCATCA 424
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190 pthrlcysrthrserscysrthrglypheproleuserthrargvalprogl 207  
 423 CAGCGCTGTCACGAGCTGCACCTGGCTCCGCCACACAGGCTACGAC 374  
 207 1yAlaGluLucysgluaArgAlaValIleaspPheValIleapheGlnasp 223  
 373 GAGCTGAGGAGGTGTAGCTGCTGCATCATGACTTGTGGCTTCCAGGAC 324  
 224 1leSerIleLysargLeuGlnArgLeuGlnAlaLeuGlnAlaProgl 240  
 323 ATCTCATCAAGAGGCTGCAGCGCTGCGACAGCCCTCGAGGCCGCCGGA 274  
 240 uGlyTrpGlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysL 257  
 273 GGGCTGGGGTCCGACACCAAGCGCGCCCGCGCTTGCAGCTCAAGAC 224  
 257 euArgArgLeuthrGlnLeuGlnArgAlaGlnaspGlyAlaLeuLeu 273  
 223 TCGCTGGGGCTGCAGGAGCTCTGGGGGCGCAGGAGCGGGCTGCTG 174  
 274 ValArgLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGluArg 290  
 173 GTCGGCTGCTGCAGCGCTGCGGCGCCAGATGCCCGGCTGAGGCG 124  
 290 gSerValArgGluArgPheLeuProValHis 300  
 123 GAGGCTCGTGCAGCGCTTCTCCCTGTCAC 93

seq\_name: gb\_est82:BF001490

seq\_documentation\_block:

LOCUS BF001490 478 bp mRNA EST 06-OCT-2000  
 DEFINITION 7988h10.x1 NCI-CGAP\_Col6 Homo sapiens cDNA clone IMAGE:3313603 3'  
 similar to contains PTRS.b1 TAR1 repetitive element ;, mRNA  
 sequence.

ACCESSION BF001490

VERSION BF001490.1 GI:10701765

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 478)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapds-remail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,  
 Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primer: -40UP from Gihco

High quality sequence stop: 419.

Location/Qualifiers

FEATURES

source

1..478

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3313603"

/clone\_lib="NCI-CGAP\_Col6"

/tissue\_type="Colon tumor, RER+"

/lab\_host="DH10B"

/note="Organ: Colon; Vector: pT7T3D-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 Plasmid DNA from the normalized library NCI-CGAP\_Col6 was  
 prepared, and as circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (cloneIDs 1057416-1061255, and 114584-114531).  
 Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 108 a 146 c 144 g 80 t

alignment\_scores:

Quality: 604.00 Length: 119

Ratio: 5.076 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-006-352-2 x BF001490/rev ..

Align seg 1/1 to reverse of: BF001490 from: 1 to: 478

182 AsnValProGlySerSerSerHisAspThrLeuCysThrSerCysThrG1 198  
 476 AATGTGCCAGGCTTCCCTCCATGACACCCCTGTGACACGCTGCACCTG 427  
 198 yPheProLeuSerThrArgValProGlyAlaGluGluCysGluArgAlaV 215  
 426 CTTCCCTCCACACAGGAGGTACAGAGCTGAGAGTGTAGAGCTGCCG 377  
 215 a11leAspPheValAlaPheGlnaspIleSerIleLysArgLeuGlnArg 231  
 376 TCATCGACTTGTGTGCTTCCAGACATCTCATCAAGAGCTGCAGCG 327  
 232 LeuLeuGlnAlaLeuGlnAlaProGlyTrpGlyProThrProArgAl 248  
 326 CTGCTGCAGGCGCTCGAGGCCCGAGGCTGGGTCCGACACCAAGGCG 277  
 248 aglyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuL 265  
 276 GGGCGCGCGGCTTGCAGCTGAACTGTGCGGCGCTCAAGAGAGCTCC 227  
 265 euGlyAlaGlnaspGlyAlaLeuLeuValArgLeuGlnAlaLeuArg 281  
 226 TGGGGCGCGAGCAGCGGCGCTGCTGTGCGGCTCTCGAGCGCTGCGC 177  
 282 ValAlaArgMetProGlyLeuGlnArgSerValArgGluArgPheLeuP 298  
 176 GTGGCCAGAGATGCCCGGCGCTGAGCGAGCGTCCGTGAGCCCTTCTCC 127  
 298 oValHis 300  
 126 TGTGAC 120

seq\_name: gb\_est42:AM083914

seq\_documentation\_block:

LOCUS AM083914 515 bp mRNA EST 14-OCT-1999

DEFINITION xc25902.x1 NCI-CGAP\_Col9 Homo sapiens cDNA clone IMAGE:2585330 3'  
 similar to TR:095407 095407 DEOY RECEPTOR 3.;, mRNA sequence.

ACCESSION AM083914

VERSION AM083914.1 GI:6039066

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 515)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapds-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life

Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The



I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
Seq primer: -400p from Gibco  
High quality sequence stop: 355.

## FEATURES

Source  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NCI-CGAP\_C019"  
/tissue\_type="moderately differentiated adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: colon; Vector: pCMV-Sport6; Site\_1: Salt;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Normalized to Cot 50. Average insert size 1.32kb.  
Normalized version of NCI-CGAP\_C018. Library constructed  
by Life Technologies." 102 a 160 c 158 g 94 t 1 others

## alignment\_scores:

Quality: 584.00 Length: 137  
Ratio: 4.598 Gaps: 0  
Percent Similarity: 92.701 Percent Identity: 92.701

## alignment\_block:

US-09-006-352-2 x AM083914/rev

Align seg 1/1 to reverse of: AM083914 from: 1 to: 515

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|||||
515 AGCTCAAGACAGTCCAGCCCGCAAAATGCGGGCCCTTGCGCTGGCGC 466
180 AlaAsnValProGlySerSerHisAspThrLeuGlySerCysT 197
|||||
465 CCGCATGTGCGCAGGCTCTTCCCAATGACACCGTGTGACACCTTCCA 416
197 htcGlyPheProLeuSerThrArgValProGlyAlaGluGlyGluGly 213
|||||
415 CTGGCTCCCTCCCTCAGCACAGGGGTACAGAGCTGAGAGTGTGCGCT 366
214 AlaValIleAspPheValAlaPheGlnAspIleSerIleLeuArgLeuG 230
|||||
365 GCGTCATGACTTGTGCTTTCAGGACAT.TCCATCAAGAGCTGCA 317
230 nargLeuGlnAlaLeuGlnAlaProGluGlyTyrPglYProThrPro 247
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264 LeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuGlnAlaLe 280
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LOCUS AM014771 459 bp mRNA EST 10-SEP-1999  
DEFINITION UI-H-BIO-aag-g-04-0-01.s1 NCI-CGAP-Sub1 Homo sapiens cDNA clone  
IMAGE:2709294 3', mRNA sequence.

ACCESSION AM014771  
VERSION AM014771.1 GI:5863528  
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Cetartata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgap@femail.nih.gov](mailto:cgap@femail.nih.gov)

The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a donated poly A  
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
Seq primer: M13 Forward  
POLY-A=yes.

## location/Qualifiers

## FEATURES

## source

1..459  
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NCI-CGAP\_P933, NCI-CGAP\_P934, NCI-CGAP\_P935, NCI-CGAP\_P936,  
NCI-CGAP\_P937, NCI-CGAP\_P938, NCI-CGAP\_P939, NCI-CGAP\_P940,  
NCI-CGAP\_P941, NCI-CGAP\_P942, NCI-CGAP\_P943, NCI-CGAP\_P944,  
NCI-CGAP\_P945, NCI-CGAP\_P946, NCI-CGAP\_P947, NCI-CGAP\_P948,  
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NCI-CGAP\_P1101, NCI-CGAP\_P1102, NCI-CGAP\_P1103, NCI-CGAP\_P1104,  
NCI-CGAP\_P110



Quality: 580.00 Length: 116  
Ratio: 5.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 98.276

## alignment\_block:

US-09-006-352-2 x AW014771/rev ..

Align seg 1/1 to reverse of: AW014771 from: 1 to: 459

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201 userThrArgValProGluAlaGluGluCysGluArgAlaValIleasp 218
|||||
407 CAGCACCAGGTACAGAGAGCTGAGAGTGTGAGCTGACCTCATGAGCT 358
218 heValAlaPheGlnAspIleSerIleLysArgLeuGlnArgLeuLeuGln 234
|||||
357 TTGTGGCTTCCAGGACATCTCCATCAAGAGCTGACGCGGTTCTCTGACG 308
235 AlaleuGlnAlaProGluGlyTrpGlyProThrProArgAlaGlyArgAl 251
|||||
307 GCCCTCCAGGCGCCGAGAGGCTGGGGTCCGACACCAAGGCGGCGCGCC 258
251 aAlaleuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGluAlaG 268
|||||
257 GGCTTCAGCTGAAGCTGCGTCCGCGGCTCAGAGAGCTCTGGGGGCGC 208
268 InaspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArg 284
|||||
207 AGGAGGCGGCGCTCTGTCGCGCTGTCGAGGCGCTGCGGTCGCCACG 158
285 MetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 300
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157 ATGCCCGGCGTGGAGCGAGCGTCCGTGAGCGTTCCTCTCTGTCAC 110
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seq\_name: gb\_est25:AI857725

## seq\_documentation\_block:

LOCUS AI857725 445 bp mRNA EST 07-MAR-2000  
DEFINITION w121a08.x1 NCI\_CGAP\_Ut1 Homo sapiens CDNA clone IMAGE:2425526 3',  
mRNA sequence.  
ACCESSION AI857725  
VERSION AI857725.1 GI:5511330  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.lnl.gov/bbrp/image/image.html  
Insert length: 1138 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence score: 418.

## FEATURES

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/clone="IMAGE:2425526"

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adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site.1: SalI;  
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Life Technologies catalog #:  
11538-014"

BASE COUNT 100 a 140 c 130 g 75 t  
ORIGIN

## alignment\_scores:

Quality: 546.00 Length: 108  
Ratio: 5.056 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-006-352-2 x AI857725/rev ..

Align seg 1/1 to reverse of: AI857725 from: 1 to: 445

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193 CysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaG 209
|||||
445 TGACACAGCTCCACTGCTCCCTCCCTCAGACACGAGTACAGAGAGCTGA 396
209 uGluCysGluArgAlaValIleaspPheValAlaPheGlnAspIleSer 226
|||||
395 GGAGGTGAGCGGTGCGCTCATCGACTTGTGGCTTCCAGGACATCTCCA 346
226 IeLysArgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrp 242
|||||
345 TCAGAGAGCTCAGAGCGGCTGCTGCGAGGCTCGAGAGCGCCGAGGGCTGG 296
243 GlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArg 259
|||||
295 GGTCCGACACCAAGGCGGCGCGGCTTGCAGCTGAAGCTGCGCTCG 246
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245 GCGGCTCAGGAGCTCCCTGGGGGCGCAGAGGCGGCTGCTGTGGTGGC 196
276 euleuGlnAlaLeuArgValAlaArgMetProGlyLeuGluArgSerVal 292
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195 TGCTGCAAGCGCTGCGCGTGGCCAGAGATGCCGCGGCTGAGCGAGCGTC 146
293 ArgGluArgPheLeuProValHis 300
|||||
145 CGTGAAGCGCTTCTCTCCCTGTGTCAC 122
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Mon Nov 5 08:22:44 2001

us-09-006-352-2.rst

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2001, 12:32:46 ; Search time 19.91 Seconds  
(without alignments)  
913.470 Million cell updates/sec

Title: US-09-006-352-2  
Perfect score: 1634  
Sequence: 1 MRALEGPQLSLCLVLALPA.....RVARMPGLERSVEREFLPVH 300

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A.Geneseq.0601:\*

- 1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:\*
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- 9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:\*
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- 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:\*
- 12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:\*
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- 14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:\*
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- 22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634	100.0	300	19	AAW66102
2	1634	100.0	300	19	AAW63622
3	1634	100.0	300	20	AAW03099
4	1634	100.0	300	20	AAV42182
5	1634	100.0	300	20	AAV17479
6	1634	100.0	300	20	AAV06817
7	1634	100.0	300	20	AAW97749
8	1634	100.0	300	20	AAW95082
9	1634	100.0	300	21	AAI19335
10	1634	100.0	300	21	AAW28559
11	1634	100.0	300	21	AAW24057

12	1634	100.0	300	21	AAW34416	Human PRO212 prote
13	1634	100.0	300	21	AAW03621	Human Fas ligand 1
14	1634	100.0	300	21	AAW97246	M68 TNF receptor 1
15	1634	100.0	300	21	AAW90357	Human tumour necro
16	1634	100.0	300	21	AAW24395	Human PRO212 prote
17	1634	100.0	300	21	AAW96596	Human FLINT. Homo
18	1634	100.0	300	22	AAW74466	Human FLINT native
19	1634	100.0	300	22	AAW71754	Human NTR3. Homo
20	1634	100.0	300	22	AAW48161	Human PRO212 poly
21	1634	100.0	300	22	AAW50903	Human PRO212 prote
22	1620	99.1	300	21	AAW77458	Human TNF receptor
23	1619	99.1	300	21	AAW19710	Human FAS ligand 1
24	1619	99.1	300	21	AAW96597	Human FLINT. Homo
25	1610	98.5	302	20	AAW42183	Human FLINT #2 pro
26	1509	92.4	300	21	AAW03623	Human Fas ligand 1
27	1502	91.9	300	21	AAW03622	Monkey Fas ligand
28	1502	91.9	300	21	AAW03624	Human Fas ligand 1
29	1491	91.2	271	20	AAW42184	Human mFLINT #1 pr
30	1491	91.2	271	21	AAW19334	A mature human Fas
31	1491	91.2	271	21	AAW19705	Human FAS ligand 1
32	1491	91.2	271	21	AAW97247	M68 TNF receptor 1
33	1491	91.2	271	21	AAW96598	Human mature FLINT
34	1491	91.2	271	22	AAW74465	Human FLINT mature
35	1487	91.0	271	21	AAW19709	Protease-resistant
36	1487	91.0	271	22	AAW74467	Human FLINT mature
37	1485	90.9	271	21	AAW96599	Human mature FLINT
38	1481	90.6	271	21	AAW19708	Protease-resistant
39	1475	90.3	271	21	AAW19706	Protease-resistant
40	1467	89.8	271	21	AAW19707	Human mFLINT #2 pr
41	1467	89.8	273	20	AAW42185	Human tumour nec
42	1362	83.4	245	20	AAW28449	Human soluble TNF
43	1177	72.0	211	21	AAW28560	Human hAP6 protei
44	1153	70.6	215	20	AAW93585	Human TNFR super
45	841	51.5	153	20	AAW22222	

#### ALIGNMENTS

RESULT 1

AAW66102 standard; Protein; 300 AA.

AC AAW66102;

XX

DT 03-DEC-1998 (first entry)

XX

DE Amino acid sequence of tumour necrosis related receptor (TR4).

XX

KW Human: tumour necrosis related receptor; TR4; agonist; antagonist;

KW Inhibition: chronic; acute; inflammation; arthritis; septicemia;

KW autoimmune disease; transplant rejection; stroke; cancer;

KW Alzheimer's disease.

XX

OS Homo sapiens.

OS

XX

PN EP861850-A1.

PD 02-SEP-1998.

PD

XX

PF 20-JAN-1998; 98EP-0300382.

PF

XX

PR 04-FEB-1997; 97US-0794796.

PR

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA

XX

PI Emery J, Tan KB, Truneh A, Young PR;

PI

XX

DR WPI: 1998-508248/44.

DR

XX

PT N-PSDB; AAV07654.

PT

New DNA encoding tumour necrosis related receptor - used to treat and prevent e.g. inflammation, arthritis, septicemia, autoimmune



PT diseases, transplant rejection, infection, stroke, ischemia, ARDS,  
PT restenosis, AIDS, bone disorders and cancer  
XX  
PS Claim 1; Fig 1; 21pp; English.  
XX  
CC This is the amino acid sequence of the human tumour necrosis related  
CC receptor (TR4) used in the method of the invention. The TR4 protein  
CC or its agonist can be used to treat a subject in need of enhanced  
CC TR4 polypeptide activity. The antagonist is used to inhibit TR4  
CC polypeptide activity. The active agents can be used for the  
CC treatment and prevention of diseases such as chronic and acute  
CC inflammation, arthritis, septicemia, autoimmune diseases, transplant  
CC rejection, stroke, cancer, Alzheimer's disease.  
XX  
SQ Sequence 300 AA;  
  
Query Match 100.0%; Score 1634; DB 19; Length 300;  
Best Local Similarity 100.0%; Pred. No. 5.8e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 mralepgpilsilclvialpalpvpavrgvaeetpypmdaetgerlvcaqcpptgtvr 60  
QY 61 PCRDSPTTCGPPRRHYTFQWNYLERCRCYNVLCGEREEARACHATHNRACRRTGFF 120  
DB 61 pcrdspttcgpprrhytqfwnylercrycnvlgereeeaarachathnacrctgtff 120  
QY 121 AAAGFLEHASCPPGAGVIAPGTPSONTOCQPCPPTFSASSSSSEOCQPHRNCTALGLA 180  
DB 121 ahaagfclahascppgagviapgtspontocpcpptfsassssseqqphrncatlgla 180  
QY 181 LNVPGSSSHDPLTSCGTGFPPLSTRVPGAECCEERAVIDFAFODISIKRLORLQALBAPE 240  
DB 181 lnvpgssshdplctscgtgfpplstrvpgaecceeravidfafodisikrlqlrlqaleape 240  
QY 241 GWCPTFRAGRALQKLRRLRTELGAQDQALVRLQALRVARMPGERSVRRFLPVH 300  
DB 241 gwcptfragralqklrrrtellgaqdgallvrlqalrvamrglersvrrflpvh 300  
  
RESULT 2  
ID AAM63622 standard; Protein; 300 AA.  
XX  
AC AAM63622;  
XX  
DT 26-OCT-1998 (first entry)  
XX  
DE Human tumour necrosis factor receptor-6 alpha protein.  
XX  
KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;  
KW endothelial cells; keratinocytes; normal prostate; apoptosis;  
KW prostate tumour tissue.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..30  
FT Protein 31..300  
FT /note="TNFR-6 alpha"  
FT Region 31..282  
FT /note="Soluble extracellular domain"  
XX  
PN MO9830694-A2.  
XX  
PD 16-JUL-1998.  
XX  
FE 13-JAN-1998; 98MO-US00153.  
XX  
PR 14-JAN-1997; 97US-0035496.  
XX

PA (HUMA-) HUMAN GENOME SCI INC.  
PI Ethner R, Feng P, Gentz RL, N1 J, Ruben SM, Yu G;  
XX  
DR WPI: 1998-399142/34.  
XX N-PSDB; AAY030985.  
XX  
PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in  
FT the diagnosis of immune system-related disorder(s)  
XX  
PS Claim 20; Fig 1; 91pp; English.  
XX  
CC The present sequence represents the human tumour necrosis factor  
CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides  
CC for the TNFR-6 beta protein (AAM63623). TNFR-6 alpha and TNFR-6 beta  
CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs  
CC are expressed in endothelial cells, keratinocytes, normal prostate and  
CC prostate tumour tissue. For a number of disorders of these cells,  
CC particularly of the immune system, substantially altered (whether  
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene  
CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta  
CC polypeptides, nucleic acids and antibodies are claimed to be useful in  
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and  
CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are  
CC also claimed to be useful for identifying ligands which may be useful  
CC in the treatment of apoptosis related disorders.  
XX  
SQ Sequence 300 AA;  
  
Query Match 100.0%; Score 1634; DB 19; Length 300;  
Best Local Similarity 100.0%; Pred. No. 5.8e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRALGPGLSLCLVLAIPALPVPVAVRGAETPTYPMDAETGERLVCAQCPPTGVOR 60  
DB 1 mralepgpilsilclvialpalpvpavrgvaeetpypmdaetgerlvcaqcpptgtvr 60  
QY 61 PCRDSPTTCGPPRRHYTFQWNYLERCRCYNVLCGEREEARACHATHNRACRRTGFF 120  
DB 61 pcrdspttcgpprrhytqfwnylercrycnvlgereeeaarachathnacrctgtff 120  
QY 121 AAAGFLEHASCPPGAGVIAPGTPSONTOCQPCPPTFSASSSSSEOCQPHRNCTALGLA 180  
DB 121 ahaagfclahascppgagviapgtspontocpcpptfsassssseqqphrncatlgla 180  
QY 181 LNVPGSSSHDPLTSCGTGFPPLSTRVPGAECCEERAVIDFAFODISIKRLORLQALBAPE 240  
DB 181 lnvpgssshdplctscgtgfpplstrvpgaecceeravidfafodisikrlqlrlqaleape 240  
QY 241 GWCPTFRAGRALQKLRRLRTELGAQDQALVRLQALRVARMPGERSVRRFLPVH 300  
DB 241 gwcptfragralqklrrrtellgaqdgallvrlqalrvamrglersvrrflpvh 300  
  
RESULT 3  
ID AAY03099 standard; Protein; 300 AA.  
XX  
AC AAY03099;  
XX  
DT 09-DEC-1999 (first entry)  
XX  
DE Human lung TNF-receptor protein.  
XX  
KW Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;  
KW detection; immunoassay; diagnosis; disease; immune system; tumour;  
KW osteogenic system; cardiovascular system; central nervous system; asthma;  
KW peripheral nervous systems; transplant incompatibility; antitumor;  
KW rheumatoid arthritis; antiasthmatic; antiarthritic.  
XX  
OS Homo sapiens.  
XX



FH Key Location/Qualifiers  
 CDS 134..1036  
 FT /\*tag= a  
 FT /product= "TNF-receptor"  
 XX  
 PN DE19809978-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 09-MAR-1998; 98DE-1009978.  
 XX  
 PR 09-MAR-1998; 98DE-1009978.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 PI Kroeger B;  
 XX  
 DR WPI: 1999-519473/44.  
 DR N-PSDB: AA209998.  
 XX  
 PT New soluble member of tumor necrosis factor receptor family, useful for  
 PT identification specific modulators and for treating disease e.g. tumors  
 PT  
 PS Claim 1; Page 8-9; 10pp; German.  
 XX  
 XX

This invention describes a novel tumour necrosis factor (TNF) receptor (I) isolated from human lung tissue. (I) is used: (i) to raise specific antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands (A), potential therapeutic agents; and (iii) therapeutically (optionally) expressed from a gene therapy vector) in conditions associated with a deficit of (I). Ab are used: (a) for qualitative or quantitative detection of (I) in standard immunoassays (for diagnosis of disease, or susceptibility, or for monitoring); and (b) as therapeutic inhibitors in cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is used: (A) for recombinant production of (I); (B) also its oligonucleotide fragments, in standard hybridization and/or amplification assays; (C) as source of antisense molecules or ribozymes; and (D) to produce transgenic animals (for studying (patho)physiology of (I)). Diseases possibly associated with under- or over-expression of (I) are those of the immune, osteogenic, cardiovascular and central or peripheral nervous systems, CC tumors, transplant incompatibility, asthma and rheumatoid arthritis. The CC products of the invention have antitumor, antiallergic and CC antiallergic activity. This sequence represents the TNF-receptor of the CC invention.  
 CC  
 XX  
 XX Sequence 300 AA:

Query Match 100.0%; Score 1634; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5,8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 YY 1 MRALBPGSLGLCLVALPALPVPVAVGVAETPTVPMRDATGTERIVCAQCPGGTFVQR 60  
 DB 1 mralepgslslclvalpalpvpavrgvaeetpvmrdatgterlvacqpggtfivr 60  
 YY 61 PCRDSPTTCGCPRRHYHGFQFWYLERCRYCNVLCGEREEEARACATTHRARCRTRGFF 120  
 DB 61 pcrdspttcgcprrhyhgfqfwylercrycnvlgereeeearacathrarcrctgff 120  
 YY 121 AHAGFCLIEHASCPPGAGVIAPTGSONTOCQPCPPTFSASSSSSSRQCOPHRMCTALGLA 180  
 DB 121 ahagfcliehascpaggvialptgsontoqpcppptfsassssssqcpshrmtalgl 180  
 YY 181 LNVPGSSSHDTCTSCCTGPEPLSTRVPVGAECERAVIDPAFODISIKRLQRLQALPAPE 240  
 DB 181 lnvpgssshdtctscctgpeplstrvpvgaecercavidvafgdisikrlqllqaleape 240  
 YY 241 GAGPTPRAGRAALQTLRLRFTLLGAOGALLVRLLOALRVARMGLERSVEREFLPVH 300  
 DB 241 gwagptpragraalqltrlrftlllgaogallvrlloalrvarmglersveretflpvh 300

RESULT 4  
 ID AA42182  
 XX AA42182 standard; Protein; 300 AA.  
 AC AA42182;  
 DE Human FLINT #1 protein sequence.  
 DT 17-DEC-1999 (first entry)  
 XX  
 XX  
 KW Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;  
 KW apoptosis; inflammation; cancer; diabetes; acute liver failure;  
 KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;  
 KW reperfusion-associated injury; aplastic anaemia; differentiation;  
 KW growth; myelodysplastic syndrome; pancytopenic condition;  
 KW myocardial ischaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0950413-A2.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 30-MAR-1999; 99WO-US06797.  
 XX  
 PR 30-MAR-1998; 98US-0079856.  
 PR 20-MAY-1998; 98US-0086074.  
 PR 09-SEP-1998; 98US-0099643.  
 PR 17-DEC-1998; 98US-0112577.  
 PR 18-DEC-1998; 98US-0112703.  
 PR 18-DEC-1998; 98US-0112933.  
 PR 22-DEC-1998; 98US-0113407.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Bimol TF, Dou S, Glasbrook AL, Gould KE, Hale JE, Heuer JG;  
 PI Hui KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;  
 PI Song HY, Wang J, Wu X, Zuckerman SH;  
 XX  
 DR WPI: 1999-591319/50.  
 DR N-PSDB: AA25375.  
 XX  
 PT Use of mature FLINT for treating acute liver failure, inflammation,  
 PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic  
 PT and proinflammatory activity  
 XX  
 PS Claim 30; Fig 1; 99pp; English.  
 XX  
 XX The present invention describes therapeutic applications of mature FLINT  
 CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT  
 CC (mFLINT), which is a member of the tumour necrosis factor receptor  
 CC superfamily, is used for treating acute liver failure, inflammation of  
 CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated  
 CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated  
 CC injury or disorder such as hypercoagulation (including use with  
 CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury  
 CC or disorder, Type I diabetes, cancer, cell damage or damage to an  
 CC innocent bystander tissue that is induced by a chemotherapeutic agent or  
 CC therapeutic irradiation, treating haematopoietic progenitor cells that  
 CC have been exposed to therapeutic radiation or chemotherapy, aplastic  
 CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is  
 CC also used for promoting the growth or differentiation of a haematopoietic  
 CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte  
 CC resulting from abnormal myocardial ischaemia. The present sequence  
 CC represents human FLINT.  
 XX  
 XX Sequence 300 AA:

Query Match 100.0%; Score 1634; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5,8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 MRALBPGSLILCTLVLPALPVPVAVRGVAETPTTPMPMDATGEBRLVCAQCPEPTVOR 60  
 Db 1 mralbpgslilctlvlpalvpavrgvaetpttpmmdatgbrlvcaqcpptvqr 60  
 QY 61 PCRDSPTTGCPGPPRHATQFMYLERCRCVNLGSEEREERACHATHNACRCRTGFF 120  
 Db 61 pcrdpspttgcpgrprrhatqfmylercrvnlgsereearachathnacrcrtgff 120  
 QY 121 AHAGFCELEHASCPPGAGVIAPGTPSQNTQCPCPGPTFSASSSSBQCQPHRNCTALGLA 180  
 Db 121 ahagfcelehascpagviapgtpsqntqcpcpgptfsassssbqcqphrncalgl 180  
 QY 181 LNPVGSSSHDTLCTGCTGFPLSTRVPGAECECERAVIDFAFODISIKRLQRLQALBAPE 240  
 Db 181 lnpvgssshdtlctgctgfpstrvpgaececeravidfafodisikrlqrlqal 240  
 QY 241 GWPPTPRAGRAALQKLRRRLTELLGAODGALLVRLLOALRYARMPGLERSVREERFLPVH 300  
 Db 241 gwpptpragraalqklrrrltelldgaodgallvrlloalryarmpglersvreflrvh 300  
 RESULT 5  
 ID AAY17479 standard; Protein; 300 AA.  
 AC AAY17479;  
 DT 02-AUG-1999 (first entry)  
 DE Mammalian tumour necrosis factor receptor OPG-2.  
 KM Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease;  
 KM osteopenic disorder; osteoclast activity; primary osteoporosis;  
 KM hyperglycaemia; osteolytic metastasis; immune response; cancer.  
 OS Mammalia.  
 PN WO9926977-A1.  
 PD 03-JUN-1999.  
 PF 24-NOV-1998; 98WO-US25065.  
 PR 17-FEB-1998; 98US-0074896.  
 PR 24-NOV-1997; 97US-0066446.  
 PA (BIOJ ) BIOGEN INC.  
 PI Tschoop J;  
 DR WPI: 1999-347693/29.  
 DR N-PSDB: AAX76052.  
 PT New tumour necrosis factor family receptor OPG-2  
 PS Claim 1; Page 18; 22pp: English.  
 XX The present sequence represents a mammalian tumour necrosis factor  
 CC receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis  
 CC factor receptor family, and can be used: (i) to raise specific  
 CC antibodies (Ab), (ii) to treat osteopenic disorders associated with  
 CC excessive osteoclast activity, e.g. primary osteoporosis, Paget's  
 CC disease, hyperglycaemia of malignancy, or osteolytic metastases; (iii)  
 CC for affinity purification of cognate ligands, and (iv) to screen for  
 CC ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents  
 CC as soluble forms of the protein, are used to prevent, or reduce  
 CC severity of, an immune response, and for treating cancer. They can also  
 CC be used in diagnostic assays. The nucleic acid sequence encoding OPG-2  
 CC can be used as a probe to isolate related sequences from other species.  
 XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;  
 Best Local Similarity 100.0%; Fred. No. 5.8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRALBPGSLILCTLVLPALPVPVAVRGVAETPTTPMPMDATGEBRLVCAQCPEPTVOR 60  
 Db 1 mralbpgslilctlvlpalvpavrgvaetpttpmmdatgbrlvcaqcpptvqr 60  
 QY 61 PCRDSPTTGCPGPPRHATQFMYLERCRCVNLGSEEREERACHATHNACRCRTGFF 120  
 Db 61 pcrdpspttgcpgrprrhatqfmylercrvnlgsereearachathnacrcrtgff 120  
 QY 121 AHAGFCELEHASCPPGAGVIAPGTPSQNTQCPCPGPTFSASSSSBQCQPHRNCTALGLA 180  
 Db 121 ahagfcelehascpagviapgtpsqntqcpcpgptfsassssbqcqphrncalgl 180  
 QY 181 LNPVGSSSHDTLCTGCTGFPLSTRVPGAECECERAVIDFAFODISIKRLQRLQALBAPE 240  
 Db 181 lnpvgssshdtlctgctgfpstrvpgaececeravidfafodisikrlqrlqal 240  
 QY 241 GWPPTPRAGRAALQKLRRRLTELLGAODGALLVRLLOALRYARMPGLERSVREERFLPVH 300  
 Db 241 gwpptpragraalqklrrrltelldgaodgallvrlloalryarmpglersvreflrvh 300  
 RESULT 6  
 ID AAY06817 standard; Protein; 300 AA.  
 AC AAY06817;  
 DT 24-JUN-1999 (first entry)  
 DE Human DCR3 polypeptide.  
 KM DCR3 polypeptide; tumour necrosis factor receptor; TNFR; Fas ligand;  
 KM apoptosis; T cell mediated immune response; allergy; asthma; cancer;  
 KM rheumatoid arthritis; Crohn's disease; guest vs. host disease; human;  
 OS Homo sapiens.  
 PN WO9914330-A1.  
 PD 25-MAR-1999.  
 PF 18-SEP-1998; 98WO-US19661.  
 PR 30-JUL-1998; 98US-00934640.  
 PR 18-SEP-1997; 97US-0059288.  
 PA (GENTH ) GENENTECH INC.  
 PI Ashkenazi AJ, Botstein D, Dodge KH, Goddard A, Gurney AL;  
 PI Kim KJ, Lawrence DA, Pilti R, Roy MA, Tumas DB;  
 PI Wood WI;  
 DR WPI: 1999-244032/20.  
 DR N-PSDB: AAX32744.  
 PT DCR3 polypeptide related to tumor necrosis factor receptor  
 PS Claim 5; Fig 1; 88pp: English.  
 XX This represents a human DCR3 polypeptide, a homologue of tumour necrosis  
 CC factor receptor (TNFR) polypeptide. Host cells containing a vector  
 CC comprising the DCR3 nucleic acid can be used for the recombinant  
 CC expression of the protein. DCR3 binds to Fas ligand, so it (or its  
 CC chimera) are useful for modulating apoptosis in mammalian cells, also  
 CC other Fas-ligand induced activities, particularly to inhibit T cell  
 CC mediated immune responses, e.g. in treatment of allergy, asthma,  
 CC rheumatoid arthritis, Crohn's disease, guest vs. host disease etc. DCR3







XX HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;  
 KW tumour necrosis factor receptor; muscle disorder; bone mass; screening;  
 KM muscle metabolism; binding agent; cognate ligand.  
 XX Homo sapiens.  
 OS  
 PN WO9907738-A2.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 04-AUG-1998; 98WO-US16202.  
 XX  
 PR 06-AUG-1997; 97US-0054869.  
 XX  
 PA (PROC.) PROCTER & GAMBLE CO.  
 PA (REG.) REGENERON PHARM INC.  
 XX  
 PI Maslakowski PJ, Morris J, Valenzuela DM;  
 XX WPI: 1999-167365/14.  
 DR N-PSDB; AAX23300.  
 XX  
 PT Novel orphan human receptor polypeptide and nucleic acid - useful as  
 PT diagnostic reagents and for treatment of muscle disorders  
 XX  
 PS Claim 7; Page 21; 23pp; English.  
 CC This represents a HUMAN NTR-1 polypeptide, a novel orphan receptor. The  
 CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor  
 CC receptor (TNFR). Host cells transformed with a vector comprising the  
 CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the  
 CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the  
 CC protein are useful for diagnosis and treatment of humans and animals,  
 CC especially muscle disorders, as the receptor is involved in regulation of  
 CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful  
 CC for screening for novel binding agents, and cognate ligands, which may be  
 CC used to treat disorders associated with HUMAN NTR-1 imbalance.  
 XX  
 SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MHAEFGSLSLCLVLAIPALPVPVAVRGVAETPTYPWRDAETGRLVCAQCPPTGFVOR 60  
 DB 1 mralegpjlslclvialpallpvpavrgvaeetpypwrdaetgerlvcaqcpptgtvqr 60  
 OY 61 PCRDSPTTCGPPRRHYTOFWNYLERCRYCNVLCGEREEARACHATNHRACRCRTGFF 120  
 DB 61 pcrdspttcgpprrhytqfwmylercrycnvlgereearachathnraactrtgff 120  
 OY 121 AHAGFCLHASCPRGAGVIAPGTPSONTOCOPCPGTSSASSSSSECCOPHRNCTALGLA 180  
 DB 121 ahagfclhascprgagviapgtpsnqlcqpccpgtlsassssccqcpmrtctaigla 180  
 OY 181 LNWPGSSSHDPLCTSCGPFPLSTRVPGAECEERAVIDVAODISIKRLORLQALEAPE 240  
 DB 181 lnpwpgsshdplctscgpfplstrvpgaeeceraavidvalqdsikrlqlqaleape 240  
 OY 241 GWGPTPAGRAAIQKLRRLTELLGAQDQALLVRLQALFVARMPCLERSVERELPYVH 300  
 DB 241 gwgpptpagraaiqlkrrlteellgaqdgallvrlqalvvarmpclersverelpyvh 300

RESULT 9  
 AABI9335  
 ID AABI9335 standard; Protein; 300 AA.  
 XX  
 AC AABI9335;  
 XX

DT 19-FEB-2001 (first entry)  
 DE A full length human FAS ligand Inhibitory Protein (FLINT).  
 XX  
 XX Human; FAS ligand Inhibitory Protein; FLINT; analogue; apoptosis;  
 KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;  
 KM acute respiratory distress syndrome; ulcerative colitis;  
 XX chronic obstructive pulmonary disease; Crohn's disease.  
 XX Homo sapiens.  
 OS  
 PN WO200058465-A2.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 20-MAR-2000; 2000WO-US06417.  
 XX  
 PR 30-MAR-1999; 99US-0126839.  
 PR 21-JUN-1999; 99US-0140077.  
 PR 21-JUN-1999; 99US-0140156.  
 PR 20-OCT-1999; 99US-0160566.  
 PR 18-FEB-2000; 2000US-0183398.  
 XX  
 PA (ELIL) LILLY & CO ELI.  
 XX  
 PI Becker GW, Cohen RJ, Gonzalez-dewhilt PA, Hale JE, Micanovic R;  
 PI Newton CM, Mobilitz JW, Ratimachalam R, Tschang SR, Wiltcher DR;  
 PI Wroblewski VJ.  
 XX  
 DR WPI: 2000-656167/63.  
 XX  
 PT FAS ligand Inhibitory Protein analogs useful for treating abnormal  
 PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,  
 PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's  
 PT disease -  
 XX  
 PS Disclosure: Page 113-114; 114pp; English.  
 XX  
 CC The present sequence represents a full length human FAS ligand Inhibitory  
 CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor  
 CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature  
 CC FLINT protein is modified to produce analogues, which have greater  
 CC potency, longer in vivo half-lives, decreased aggregation, decreased  
 CC absorption onto surfaces, increased solubility and improved ease of  
 CC formulation. The FLINT analogue is useful for treating a patient  
 CC suffering from disease or condition relating to abnormal apoptosis such  
 CC as acute lung injury, acute respiratory distress syndrome, pulmonary  
 CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or  
 CC Crohn's disease.  
 XX  
 SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MHAEFGSLSLCLVLAIPALPVPVAVRGVAETPTYPWRDAETGRLVCAQCPPTGFVOR 60  
 DB 1 mralegpjlslclvialpallpvpavrgvaeetpypwrdaetgerlvcaqcpptgtvqr 60  
 OY 61 PCRDSPTTCGPPRRHYTOFWNYLERCRYCNVLCGEREEARACHATNHRACRCRTGFF 120  
 DB 61 pcrdspttcgpprrhytqfwmylercrycnvlgereearachathnraactrtgff 120  
 OY 121 AHAGFCLHASCPRGAGVIAPGTPSONTOCOPCPGTSSASSSSSECCOPHRNCTALGLA 180  
 DB 121 ahagfclhascprgagviapgtpsnqlcqpccpgtlsassssccqcpmrtctaigla 180  
 OY 181 LNWPGSSSHDPLCTSCGPFPLSTRVPGAECEERAVIDVAODISIKRLORLQALEAPE 240  
 DB 181 lnpwpgsshdplctscgpfplstrvpgaeeceraavidvalqdsikrlqlqaleape 240



QY 241 GNGPTPRAGRAALQKLRRLTELLGAQDGLLVRLQLARVARMPGLERSVERFLPVH 300  
 DB 241 gwgpptpragraalqlklrrltelllgagdgallvrlqlalvarmpglersverflpvh 300

RESULT 10

ID AAB28559 standard; protein; 300 AA.

AC AAB28559;

DT 08-FEB-2001 (first entry)

DE Human soluble TNF receptor tnfrsf-1.

XX Human: tumour necrosis factor like-1; TNF1; tumour necrosis factor; TNF;  
 KM immunosuppressive; antihistaminic; neuroprotective; dermatological;  
 KM antiinflammatory; antidiabetic; cyostatic; osteophtic; gene therapy;  
 KM colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;  
 KM osteoporosis; autoimmune disease; myasthenia gravis;  
 KM insulin-dependent diabetes mellitus.

OS Homo sapiens.

PN MO200060079-A2.

PD 12-OCT-2000.

PF 05-APR-2000; 2000MO-US09058.

PR 05-APR-1999; 99US-0286529.

PA (CHIR ) CHIRON CORP.

PI Tribouley C;

DR WPI: 2000-665004/64.

DR N-PSDB: AAC63764.

PT Tumour necrosis factor (TNF) and TNF receptor superfamily protein  
 PT members TNF-L and TNFR-L, useful for enhancing or decreasing TNF  
 PT activities such as inducing cell death and lymphoid organogenesis -  
 PS Claim 1: Page 72; 77pp; English.

XX The present sequence is given in a specification relating to an isolated  
 CC human protein designated tumour necrosis factor like-1 (TNFL1). It may be  
 CC used to induce cell death in tumours, to induce apoptosis of activated T  
 CC cells, to induce inflammation, and to rescue resting T cells from  
 CC apoptosis. TNF receptors are used to regulate the function of a TNF  
 CC ligand which plays a role in apoptosis, inflammation, differentiation, or  
 CC proliferation. Expression of the receptors can also be useful as markers  
 CC for cancer, especially for colon cancer. Diseases which can be treated  
 CC using ligands and/or receptors of the TNF/TNFR superfamily include  
 CC rheumatoid arthritis, cancer, septic shock, Crohn's disease and  
 CC osteoporosis. The polynucleotides can be used in gene delivery vehicles,  
 CC for the purpose of delivering a mRNA or oligonucleotide, full-length  
 CC protein, fusion protein, polypeptide, or ribozyme, or single-chain  
 CC antibody, into a cell. The newly identified receptor proteins play  
 CC regulatory roles in cell proliferation and/or differentiation. The  
 CC receptors can also play a role in the negative regulation of  
 CC osteoclastogenesis. Soluble TNFR-like receptors can be useful in the  
 CC neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be  
 CC used to treat autoimmune diseases (myasthenia gravis and  
 CC insulin-dependent diabetes mellitus), tumours, and proliferative  
 CC disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be  
 CC delivered to subjects for the purpose of screening test compounds for  
 CC those which are useful for enhancing transfer of TNF-L subgenomic  
 CC polynucleotides to the cell or for enhancing subsequent biological  
 CC effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.  
 XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5,8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLEGGSLTCLVIALPALLPVPVAVRGVAFETPYPMRAEGERLYVCAQCPEPGFVOR 60  
 DB 1 mraleppgsllclvialpalpvpavrgvaeetpyvwdaetgerlyvcaqcpptfvtqr 60  
 QY 61 PCRDSPTTCGPPRRHYTFYFMVYLERCRCNVLCGEEREERACHATHRACRCRTGFF 120  
 DB 61 pcrdspttcgpprrhytqfwylercyrcnvlcgereeerachathrractrtgff 120  
 QY 121 AHAGFCLHNASCPGAGVIAFGTPSQNTQCPQPPGTFSSASSSSSQCCPHRNCTALGLA 180  
 DB 121 ahagfclenascpagvialfgtspqntqcpqppgtfssasssssqcphrncalgl 180  
 QY 181 LNPVSSSHHTLTCTSCGFPLSTRVGAECCEBAVIDFAFQDISIKRLQRLQALEAPE 240  
 DB 181 lnpvssshhtlctscgfpplstrvgaeccebaividfafqdisikrlrlqaleape 240  
 QY 241 GNGPTPRAGRAALQKLRRLTELLGAQDGLLVRLQLARVARMPGLERSVERFLPVH 300  
 DB 241 gwgpptpragraalqlklrrltelllgagdgallvrlqlalvarmpglersverflpvh 300

RESULT 11

ID AAB24057 standard; protein; 300 AA.

AC AAB24057;

DT 29-JAN-2001 (first entry)

DE Human PRO212 protein sequence SEQ ID NO:2.

XX Human: tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 KM proliferation; tumorigenesis; identification; cancer; cyostatic;  
 KM neurotropic; neuroprotective; antiinflammatory; immunosuppressive;  
 KM immunostimulant; antiangiogenic; leukemia; lymphoid malignancy;  
 KM neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
 KM hypothalamic disorder; glandular disorder; macrophagal disorder;  
 KM epithelial disorder; stromal disorder; blastocelic disorder;  
 KM inflammatory disorder; immunologic disorder.

OS Homo sapiens.

PN MO200053755-A2.

PD 14-SEP-2000.

PF 06-JAN-2000; 2000MO-US00376.

PR 08-MAR-1999; 99MO-US05028.

PR 02-JUN-1999; 99MO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 26-JUL-1999; 99US-0145698.

PR 30-NOV-1999; 99MO-US28313.

PR 20-DEC-1999; 99MO-US30911.

PR 05-JAN-2000; 2000MO-US00219.

PA (GENE ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA,  
 PI Watanabe CK, Wood WI;  
 DR WPI: 2000-572270/53.  
 DR N-PSDB: AAC58367.  
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 PT treatment, diagnosis and prevention of cancer -  
 XX



PS Claim 61: Fig 2: 286pp: English.

XX The present invention describes an isolated antibody that binds to  
CC of the human PRO proteins designated PRO242, PRO290, PRO341, PRO535,  
CC PRO615, PRO117, PRO809, PRO830, PRO848, PRO945, PRO1005, PRO1009,  
CC PRO1023, PRO1030, PRO1039, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
CC PRO1187, PRO1261, PRO1293, PRO139, PRO834, PRO1317, PRO1710, PRO2094,  
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
CC growth. The PRO polypeptides and nucleotides are useful in the  
CC treatment, diagnosis and prevention of cancer. The antibodies and other  
CC anti-tumour compounds may be used to treat various conditions, including  
CC those characterised by overexpression and/or activation of the amplified  
CC PRO genes. Exemplary conditions or disorders to be treated with such  
CC antibodies and other compounds include benign or malignant tumours  
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),  
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,  
CC glioma, astrocytoma, hypopharyngeal and other glandular, macrophagal,  
CC epithelial, stromal and blastocoele disorders, and inflammatory,  
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
CC primers and hybridisation probes used in the isolation of the human PRO  
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
CC PRO polynucleotide and protein sequences given in the exemplification of  
CC the present invention.

Sequence 300 AA:

Query Match 100.0% Score 1634: DB 21: Length 300:  
Best Local Similarity 100.0%: Pred. NO. 3.8e-122:  
Matches 300: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 MRALEPGSLICLVLPALPPLVPAVKGVAETPTYPMDAETGEBRLVACQCPPTFFVOR 60  
DB 1 mralpgslilclvlpalplpvavtgvaeetpypmdaetgbrlvcacqcpptffvgr 60  
QY 61 PCRDSPTTCGCPRRHYTFPMYTERCKRYCNVLCGEREBERACNATHNRACKRTGTF 120  
DB 61 pcrdspttcgcprrhytftmylercrycnvlcgereeearchthnrackrtctgft 120  
QY 121 AHAGCTLEHASCPGACVIAPTGPTSONTCQCPPTGTSASSSSSECOCPHMCNTALGUA 180  
DB 121 ahagctlehascpgacvialptgptsontcqcpptgtsassssseqcqhmcntalglia 180  
QY 121 LNVGSSSHDITCTGCTGFPSTRVPAEGERAVIDVAFODSIRLQRLQALAEPE 240  
DB 121 lnvgssshdtictgctgfpstrvpaegercravivdvafodsisrllqrlqaleape 240  
QY 181 INVPGSSHDITCTGCTGFPSTRVPAEGERAVIDVAFODSIRLQRLQALAEPE 240  
DB 181 invpgsshditctgctgfpstrvpaegercravivdvafodsisrllqrlqaleape 240  
QY 241 GWCPTPRAGRAALOLKRRRLTELGAODGALLVRLQALVAPMPGLERSVRRFPVPH 300  
DB 241 gwcptpragraalolkrrrltelglaodgallvrlqalvampglersvrrfplph 300

RESULT 12

AAB33416

ID AAB33416 standard: Protein: 300 AA.

AC AAB33416:

DT 29-JAN-2001 (first entry)

XX Human PRO212 protein UNQ186 SEQ ID NO:14.

XX Human: immune related disease; diagnosis; antiinflammatory; cardiant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; noctropic; neuroprotective;  
KW antianaemic; hepatotropic; virucide; antiparasitic; antiallergic;  
KW antianaemic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW autoimmune vasculitis; autoimmune hemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopenia; immune-mediated renal disease;

KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease.  
XX Homo sapiens.  
PN WO200053758-A2.  
PD 14-SEP-2000.  
XX 02-MAR-2000: 2000WO-US05841.  
PF 08-MAR-1999: 99WO-US05028.  
PR 10-MAR-1999: 99US-0123618.  
PR 12-MAR-1999: 99US-0123957.  
PR 23-MAR-1999: 99US-0125775.  
PR 12-APR-1999: 99US-0128849.  
PR 20-APR-1999: 99WO-US08615.  
PR 28-APR-1999: 99US-0131445.  
PR 04-MAY-1999: 99US-0132371.  
PR 14-MAY-1999: 99US-0134287.  
PR 02-JUN-1999: 99WO-US12252.  
PR 23-JUN-1999: 99US-0141937.  
PR 20-JUL-1999: 99US-0141978.  
PR 26-JUL-1999: 99US-0145638.  
PR 28-JUL-1999: 99US-0146222.  
PR 01-SEP-1999: 99WO-US20111.  
PR 08-SEP-1999: 99WO-US20534.  
PR 13-SEP-1999: 99WO-US20944.  
PR 15-SEP-1999: 99WO-US21090.  
PR 15-SEP-1999: 99WO-US21547.  
PR 05-OCT-1999: 99WO-US23089.  
PR 29-OCT-1999: 99US-0162506.  
PR 29-NOV-1999: 99WO-US28214.  
PR 30-NOV-1999: 99WO-US28313.  
PR 30-NOV-1999: 99WO-US28409.  
PR 01-DEC-1999: 99WO-US28301.  
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PR 02-DEC-1999: 99WO-US28551.  
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PR 16-DEC-1999: 99WO-US30095.  
PR 20-DEC-1999: 99WO-US30999.  
PR 30-DEC-1999: 99WO-US31274.  
PR 05-JAN-2000: 2000WO-US00219.  
PR 06-JAN-2000: 2000WO-US00277.  
PR 06-JAN-2000: 2000WO-US00376.  
PR 11-FEB-2000: 2000WO-US03565.  
PR 18-FEB-2000: 2000WO-US04341.  
PR 18-FEB-2000: 2000WO-US04342.  
PR 22-FEB-2000: 2000WO-US04414.  
XX (GENTH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
PI Stewart TA, Tumas D, Watanabe CK, Wood WL, Yan M;  
XX WPI: 2000-572271/53.  
XX N-PSDB: AAC58581.  
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
XX Claim 33: Fig 6: 309pp: English.  
XX The present invention describes sixty four human PRO proteins which can  
CC be used in the treatment of immune related diseases. The human PRO  
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
CC treating and diagnosing immune related disorders. The disorders are



CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
CC autoimmune or immune-mediated skin diseases, allergic diseases,  
CC immunological diseases of the lung, and transplantation associated  
CC diseases including graft rejection and graft-versus-host-disease.  
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
CC AAB3444 to AAB3477 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
XX

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OY PCRBDSPPTGCGPCPPRHYYQFMWYLERCRVCNVLGGEREEAARACHATHRARCRRTGFF 120  
DB 61 pcrbdspptcgpcpprhyqfmylercrycnvlgereeeaaachathrarcrctgff 120  
OY 121 AHAGFCLENHACPPGAGVIAVGPSPQNTQCPCPPGTFSSASSSSSECCQPHRNCTALGIA 180  
DB 121 ahagfclenascpaggvialvpgspntqpcppgtfssassssseqcqhrrnctalgi 180  
OY 181 LNVPGSSSHDTLCTSGTGFPLSTRVPGAECEBAVIDEVAFODISIKRIQLQALAEAP 240  
DB 181 lnvpgssshdtlctscgtgfpflstrvpgaeceavidfvaqdisikrlqilqaleape 240  
OY 241 GMSGPTPRAGRAALQIKLRRLTETLLGADGALLVRLQLARVARMGLESVREERLPVH 300  
DB 241 gmsgptpragraaalqiklrrltetllgagdgallvrlqlarvarmpglesvrerflpvh 300

### RESULT 13

AAB03621  
ID AAB03621 standard; Protein; 300 AA.  
XX

AC AAB03621;

DT 03-JAN-2001 (first entry)  
XX

DE Human Fas ligand inhibitor FLINT.  
XX

XX Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;  
KW inflammation; infectious disease; ischaemia; Alzheimer's disease;  
KW Parkinson's disease; Crohn's disease; transplantation.  
XX

OS Homo sapiens.  
XX

XX key Location/Qualifiers  
FH Peptide 1..29  
FT /label= signal\_peptide  
FT Protein 30..300  
FT /label= mature\_FLINT  
FT Domain 1..42  
FT /label= domain\_1  
FT 43..85  
FT /label= domain\_2  
FT 86..122  
FT /label= domain\_3  
FT 123..165  
FT Domain /label= domain\_4  
FT

XX  
PN MO200034782-A1.  
XX  
PD 15-JUN-2000.  
XX  
PF 07-DEC-1999; 99MO-US28696.  
XX  
PR 09-DEC-1998; 98US-0111575.  
PR 09-DEC-1998; 98US-0111580.  
PR 07-JAN-1999; 99US-0115069.  
XX  
PA (ELIL ) LILLY & CO ELI.  
XX  
PI Rostock PRJ, Song HY, Su EW;  
XX  
DR N-PSDB; AAA53208.  
XX  
PT Novel monkey Fas ligand inhibitor polypeptides, useful for treating  
PT inflammatory or autoimmune disease such as rheumatoid arthritis,  
PT infectious diseases such as chronic hepatitis, and  
PT ischaemia/Re-perfusion conditions -  
XX  
PS Claim 19; Page 91-93; 101pp; English.

CC The present sequence is the protein sequence of the human Fas ligand  
CC inhibitor (FLINT). The FLINT protein is involved in cell-specific  
CC apoptosis, and can be used to treat inflammatory and autoimmune diseases  
CC such as rheumatoid arthritis, inflammatory bowel disease,  
CC graft-versus-host disease, diabetes, psoriasis and Graves' disease,  
CC infectious diseases such as HIV-induced lymphopenia, fulminant viral  
CC hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated  
CC ulceration, ischaemia and reperfusion conditions including acute  
CC myocardial infarction, acute coronary syndrome, congestive heart failure  
CC and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung  
CC injury and acute respiratory distress syndrome, Crohn's disease, brain  
CC trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic  
CC anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and  
CC multiple sclerosis. In addition, the protein and its gene can be used to  
CC prevent apoptosis following organ transplantation.  
XX

Sequence 300 AA:

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best Local Similarity 100.0%; Pred. No. 5,8e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 61 PCRBDSPPTGCGPCPPRHYYQFMWYLERCRVCNVLGGEREEAARACHATHRARCRRTGFF 120  
DB 61 pcrbdspptcgpcpprhyqfmylercrycnvlgereeeaaachathrarcrctgff 120  
OY 121 AHAGFCLENHACPPGAGVIAVGPSPQNTQCPCPPGTFSSASSSSSECCQPHRNCTALGIA 180  
DB 121 ahagfclenascpaggvialvpgspntqpcppgtfssassssseqcqhrrnctalgi 180  
OY 181 LNVPGSSSHDTLCTSGTGFPLSTRVPGAECEBAVIDEVAFODISIKRIQLQALAEAP 240  
DB 181 lnvpgssshdtlctscgtgfpflstrvpgaeceavidfvaqdisikrlqilqaleape 240  
OY 241 GMSGPTPRAGRAALQIKLRRLTETLLGADGALLVRLQLARVARMGLESVREERLPVH 300  
DB 241 gmsgptpragraaalqiklrrltetllgagdgallvrlqlarvarmpglesvrerflpvh 300

### RESULT 14

AA97246  
ID AA97246 standard; Protein; 300 AA.  
XX



AC AA197246;  
XX 19-DEC-2000 (first entry)  
DE M68 TNF receptor related protein.  
XX M68: tumour necrosis factor; TNF; programmed cell death; apoptosis;  
KW receptor; immune response; cell differentiation; ligand; cancer;  
KW bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;  
KW Grave's disease; idiopathic myxedema; autoimmune diabetes;  
KW thrombotic thrombocytopenic purpura; multiple sclerosis;  
KW liver diseases; autoimmune gastritis; ulcerative colitis;  
KW glomerulonephritis; pulmonary fibrosis; heart failure;  
KW atherosclerosis; aplastic anaemia; myelodysplastic syndromes;  
KW osteoporosis; Alzheimer's disease; Parkinsons disease; stroke;  
KW myocardial infarction; human.  
XX Homo sapiens.  
OS WO20046247-A1.  
XX 10-AUG-2000.  
PD 04-FEB-2000; 2000WO-US03037.  
XX 05-FEB-1999; 99US-0118902.  
PR 20-DEC-1999; 99US-0172754.  
XX (MERI ) MERCK & CO INC.  
XX Bai C;  
XX WPI: 2000-506066/45.  
DR N-PSDB: AAA33800, AAA53801, AAA53802.  
XX Isolated human M68 nucleic acids and proteins which are part of the  
PT tumor necrosis factor receptor (TNFR) family, useful for identifying  
PT modulators that may be used to treat various diseases e.g. cancer,  
PT osteoporosis, Alzheimer's disease  
XX  
PS Claim 1: Page 75-76; 80pp; English.  
XX The M68 protein is a member of a family of proteins which have  
CC roles in immune responses, cell death, cell proliferation and  
CC stimulation of cell differentiation. M68 lacks a transmembrane domain  
CC and is a secreted factor suggesting that it functions as a natural  
CC inhibitor for its ligand. The altered expression pattern of M68 in a  
CC multitude of tissues suggests that M68 may play a role in cancer by  
CC binding to its ligand and blocking apoptotic cell death induced by  
CC such a ligand. This anti-apoptotic role of M68 suggests that  
CC modulators of M68 will be useful in treatment of apoptosis-related  
CC diseases such as various forms of cancer and various bone disorders.  
CC M68 nucleic acids and proteins are therefore useful for treating  
CC conditions involving atypical apoptosis and for identifying  
CC modulators of M68. Modulators of M68 are useful for treatment of  
CC cancer and other diseases associated with abnormal levels of  
CC apoptosis including systemic lupus erythematosus, Hashimoto's  
CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune  
CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,  
CC liver diseases, autoimmune gastritis, ulcerative colitis,  
CC glomerulonephritis, pulmonary fibrosis, heart failure,  
CC atherosclerosis, aplastic anaemia, myelodysplastic syndromes,  
CC osteoporosis, Alzheimer's disease, Parkinsons disease, stroke, and  
CC myocardial infarction.  
XX  
SO Sequence 300 AA:

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best Local Similarity 100.0%; Pred. No. 5,8e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRALEGGSLICVLALPALLPVPVRGVATETPTYPWRDAETGERLVCACQCPPTGVOR 60

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OY 61 PCRDSPTTCGFCPPRRHYTOFWNLYLERCRCNVLCGEREEARACATHNACGCRGFE 120  
Db 61 pcrdspttcgfcpprrhytqfwmylecrynvcgereeearachahmacrcrtgff 120  
OY 121 AAAGCIELEHASCIPGAGVIAPGTPSOMTCOCPCPPTFSASSSSSEOCQPRNCTAIGLA 180  
Db 121 aaagcilehascipgagviapgpsqntqpcppptfssaasssqcqpnrnctaigla 180  
OY 181 LNVPGSSSHDTLCSTCGFPLSTFRVPGAECEERAVIDVAFODISIKRLOALQALEAPE 240  
Db 181 lnvpgssshdtlcsctcgfpilstfrvpgaeceeravidvafqdsikrlqlqaleape 240  
OY 241 GWGPTPRAGRAALQKLRRLTELLAGODGALLVRLQALRYARMPGLERSVREPRIPVH 300  
Db 241 gwgptpragraalqkrrrltelagdgallvrllqalryarmpglersvverfipvh 300  
  
RESULT 15  
AA190357  
ID AA190357 standard; Protein: 300 AA.  
XX  
AC AA190357;  
XX  
DE 04-DEC-2000 (first entry)  
XX  
DE Human tumour necrosis factor receptor-6 alpha protein sequence.  
XX  
DE Human: Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;  
KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;  
KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;  
KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;  
KW thyroid associated ophthalmopathy; cell damage; parasitic infection;  
KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;  
KW neurodegenerative disorder; Alzheimer's disease; immune disorder;  
KW graft rejection; rheumatism; liver disease; autoimmune diabetes;  
KW psoriasis; septic shock; ulcerative colitis; therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200052028-A1.  
XX  
PD 08-SEP-2000.  
XX  
PF 03-MAR-2000; 2000WO-US05686.  
XX  
PR 04-MAR-1999; 99US-0121774.  
PR 12-MAR-1999; 99US-0124092.  
PR 27-APR-1999; 99US-0131279.  
PR 30-APR-1999; 99US-0131664.  
PR 02-AUG-1999; 99US-0146371.  
PR 01-DEC-1999; 99US-0168235.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Gentz RL, NI J, Ebner R, Yu G, Ruben SM, Feng P.  
XX  
DR WPI: 2000-572174/53.  
DR N-PSDB: AAA37772.  
XX  
XX Nucleic acids encoding human tumour necrosis factor receptor (TNFR)  
PT proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.  
PT Alzheimer's disease, osteoporosis and graft rejection  
XX  
PS Claim 20; Fig 1; 332pp; English.  
XX  
XX This sequence represents the human tumour necrosis factor receptor 6  
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA  
CC and protein sequences can be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate TNFR expression. The  
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against



CC them may be used for the treatment of a range of conditions such as  
CC disorders associated with neovascularisation (especially ocular  
CC neovascularisation) (such as solid tumours and malignancies (e.g.  
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy  
CC and pre-maturity macular degeneration), allergies, inflammation,  
CC thyroid associated ophthalmopathy tissue/cell damage, wounds, microbial  
CC and parasitic infections, bone disease (e.g. osteoporosis),  
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),  
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune  
CC disorders (e.g. graft rejection), rheumatism, liver disease,  
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative  
CC colitis.  
XX  
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best local Similarity 100.0%; Pred No. 5.8e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 pcrdspttcgcppprhytqfwnylercrycnvlgereearachathnrcrcrtgff 120  
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Search completed: October 31, 2001, 12:38:44  
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ACCESSION AX082868
VERSION AX082868.1 GI:13184802
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Hsu,H.
TITLE Ntr3, a member of the tnf-receptor supergene family
JOURNAL Patent: WO 0110908-A 1 15-FEB-2001;
Amgen Inc. (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Tunney,D., Herbert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tunney,D., Matanabe,C.K. and Wood,W.I.
COMPOSITIONS AND METHODS for the treatment of immune related
diseases
Patent: WO 0073452-A 3 07-DEC-2000;
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TITLE JOURNAL
Genentech, Inc. (US)
location/Qualifiers
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VERSION AX056645.1 GI:12309639
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DEFINITION Homo sapiens decoy receptor 3 (Dcr3) mRNA, complete cds.
ACCESSION AF104419
VERSION AF104419.1 GI:4106877
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 1114)
Pilti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,
Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,
Goddard,A.D., Botstein,D. and Ashkenazi,A.
Genomic amplification of a decoy receptor for Fas ligand in lung
and colon cancer
Nature 396 (6712), 699-703 (1998)
JOURNAL
MEDLINE 99087326
REFERENCE
2 (bases 1 to 1114)
Pilti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
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Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,
Goddard,A.D., Botstein,D. and Ashkenazi,A.
Direct Submission
Submitted (04-NOV-1998) Molecular Oncology, Genentech, 1 DNA Way,
San Francisco, CA 94080, USA
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ACCESSION   AF217793
VERSION     AF217793.1   GI:6969260
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SOURCE      human.
ORGANISM    Homo sapiens

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REFERENCE
AUTHORS      Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
              Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
              Caskey,C.T.
TITLE        Overexpression of M68/DCR3 in human gastrointestinal tract tumors
              independent of gene amplification and its location in a four-gene
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JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
MEDLINE      20122600
PUBMED       10655513
REFERENCE    2 (bases 1 to 1428)
AUTHORS      Bai,C.
TITLE        Direct Submission
JOURNAL      Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,
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VERSION AX093178.1 GI:13509626  
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REFERENCE  
1 (bases 1 to 936)  
AUTHORS Atkinson,P.R., Tian,Y. and Wlcher,D.R.  
TITLE Flint proteins and formulations thereof  
JOURNAL Patent: WO 0118041-A 3 15-MAR-2001;  
Eli Lilly AND COMPANY (US)  
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SOURCE      human.
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AUTHORS     Atkinson, P.R., Tian, Y. and Wlitcher, D.R.
TITLE       Flint analog compounds and formulations thereof
JOURNAL     Patent: WO 0118055-A 3 15-MAR-2001;
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seq_documentation_block:
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DEFINITION Sequence 3 from Patent WO0118202.
ACCESSION  AX098029
VERSION     AX098029.1  GI:13514890
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 936)
AUTHORS     Atkinson, P.R., Tian, Y. and Wlitcher, D.R.
TITLE       Flint analog compounds and formulations thereof
JOURNAL     Patent: WO 0118202-A 3 15-MAR-2001;
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DEFINITION Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68,
            and ADP-ribosylation factor related protein 1 (ARRRP1) genes,
            complete cds.
ACCESSION   AF217796
VERSION     AF217796.1
KEYWORDS    GI:7012928
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 114793)
            Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
            Sandg,V., Soderman,A., Galloway,S.M., Liu,Q., Austlin,C.P. and
            Caskey,C.T.
            Overexpression of M68/DCR3 in human gastrointestinal tract tumors
            independent of gene amplification and its location in a four-gene
            cluster
            Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
JOURNAL     MEDLINE
PUBMED      20122600
            10655513
            2 (bases 1 to 114793)
            Bai,C., Metzker,M.L., Liu,X. and Caskey,C.T.
            Direct Submission
            Submitted (20-DEC-1999) WP26A-1000, Merck Research Laboratories,
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LOCUS	Accession	Size	Species	Date
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DEFINITION	Human DNA sequence from clone R4-583p15 on chromosome 20 contains ESTs, STRs, GSSs and ten CpG islands. Contains the INR58p8 gene for tumor necrosis factor receptor 6b (decoy), the 3' part of the KIAA1088 gene, the ARPP1 gene for ADP-ribosylation factor related protein 1, two genes for novel proteins, the gene for a G10p4 enhancer factor and the gene for a novel zinc finger protein similar to rat RIN 2F and the gene for a novel BTF/POZ domain containing zinc finger protein, complete sequence.			

ACCESSION AL121845  
VERSION AL121845.20 GI:8246778  
KEYWORDS HTG; ADP-ribosylation factor; ARFRP1; BTB; CpG island; GLUT4  
enhancer; KIAA1088; Poz; TNFRS6B; tumor necrosis factor; zinc  
finger.  
SOURCE human.

SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE  
1 (bases 1 to 120917)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

**AUTHORS** Matthews, L.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (05-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire

COMMENT  
CB10 1SA, UK. E-mail enquiries: [hunquery@anger.ac.uk](mailto:hunquery@anger.ac.uk) Clone requests: [clonerequest@anger.ac.uk](mailto:clonerequest@anger.ac.uk)  
On Jun 4, 2000 this sequence version replaced [gi:8052256](#).

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EM, EMBL; SW, SWISSPROT; IT, TrEMBL; WP, WormPEP; Information on the WormPEP database can be found at <http://www.sanger.ac.uk/Projects/Celegans/wormpep> This sequence was generated from part of bacterial clone contigs of human Chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/chr20>

This sequence is the entire insert of clone RP4-583p15. The true left end of clone RP5-824A14 is at 27658 in this sequence. The true right end of clone CPD-318A7 is at 48631 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems; at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP4-583p15 is from the library RPCT-4 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
vector: pCYPAC2.

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Seq Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

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134 rGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCys 150
401 CTGGTGGCGGGCTGATTGGCCCCGGGCGACCCCGACCGACGAGAACGCA 450
151 GlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluG 167
451 CAGCGGTGGCGGCGGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 500
167 nCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValP 184
501 GTGCCGCGCCACGCGACGCTGACGGCGCTGGCGCGCTGGCGCTGACATG 550
184 rGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPhePro 200
551 CAGGCTTCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 600
201 LeuSerThrArgValProGlyAlaGluGluCysGluArgAlaValIleAs 217
601 CTCACACACAGAGGTACAGAGGAGGAGAGTGTGACCGTGGCTGATGGA 650
217 pPheValAlaPheGlnAspIleSerIleLeuArgLeuGlnArgLeuLeuG 234
651 CTCTTGGCTTTCAGGACATCTCCATCAAGAGCGTGCAGCGCGTGTGC 700
234 IAlaLeuGluAlaProGluGlyThrGlyProThrProArgAlaGlyArg 250
701 AAGGCGCTGAGGCGCGGAGGGGCTGGGCTGCAGACACCAAGAGGCGGCG 750

```

```

251 AlaAlaLeuGlnLeuIlysLeuArgArgArgLeuThrGlnLeuLeuGlyAl 267
751 GCGGCTTTCAGGCTGAGAGCTGGCTGGCGCTGCACGAGAGCTCCTGGGGGC 800
267 aGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaA 284
801 GCAGAGCGGCGGCGCTGGCTGGCGCTGGCTGGCTGGCTGGCTGGCTGGC 850
284 rGmetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 300
851 GGATGCCCGGGCTGAGGCGGAGCGTCCGTGAGCGCTCTCTCCCTGTGTGAC 900

seq_name: /SIDSI/gcgdata/geneseq/geneseqn/AA2000.DAT:AA53208
seq_documentation_block:
ID AA53208 standard; cDNA; 900 BP.
XX
AC AA53208;
XX
DE 03-JAN-2001 (first entry)
XX
DE Human Fas ligand inhibitor FLINT coding sequence.
XX
KW Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
KW Inflammation; infectious disease; Ischemia; Alzheimer's disease;
KW Parkinson's disease; Crohn's disease; transplantation; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..900
FT /tag= a
FT /product= "FLINT"
FT /partial
FT sig_peptide 1..90
FT /tag= b
FT mat_peptide 91..900
FT /tag= c
XX
PN MO200034782-AL.
XX
PD 15-JUN-2000.
XX
PE 07-DEC-1999; 99WO-0528696.
XX
PR 09-DEC-1998; 98US-0111575.
PR 09-DEC-1998; 98US-0111580.
PR 07-JAN-1999; 99US-0115069.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Rosteck PR1, Song HY, Su EW;
XX
DR WPI: 2000-431379/37.
XX P-PSDB: AAB03621.
XX
PT Noyel monkey Fas ligand inhibitor polypeptides, useful for treating
PT inflammatory or autoimmune disease such as Rheumatoid arthritis,
PT infectious diseases such as chronic hepatitis, and
PT Ischemia/Re-perfusion conditions -
XX
PS Example 1; Page 88-91; 101pp; English.
XX
CC The present sequence is the coding sequence of the human Fas ligand
CC inhibitor (FLINT). The FLINT protein is involved in cell-specific
CC apoptosis, and can be used to treat inflammatory and autoimmune diseases
CC such as rheumatoid arthritis, inflammatory bowel disease,
CC graft-versus-host disease, diabetes, psoriasis and Graves' disease,
CC infectious diseases such as HIV-induced lymphopenia, fulminant viral
CC hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
CC ulceration, ischemia and reperfusion conditions including acute
CC myocardial infarction, acute coronary syndrome, congestive heart failure
CC and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung

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Quality: 1634.00 Length: 300  
 Ratio: 5.447 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-006-352-2 x AAF62705

Align seg 1/1 to: AAF62705 from: 1 to: 1055

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1 MetAFAAlaLeuGluGlyProGlyLeuSerLeuLeuValLeuAl 17
67 ATGAGGGCGCTGAGAGGCGCAGGCGCTGCTGCTGCTGCTGCTG 116
17 AlaProAlaLeuLeuProAlaValArgGlyValAlaGluThrP 34
117 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 166
34 rothryProtrrPAqAPAlaGluThrGlyGluArgLeuValCysAla 50
167 CCACCTACCCCTGGGGGAGCGAGAGAGAGGAGCGGCTGCTGCTG 216
51 GlucyProProGlyThrPheValGluArgProCysArgArgAspSerPr 67
217 CAGTGGCCCCAGGACCTTTGTGACGCGCCGCTGCTGCTGCTGCTG 266
67 oThrPrCysGlyProCysProProAlaGlyIstYrThrGlnPheTrpAsnT 84
267 CAGCAGCTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 316
84 yrluGluArgCysArgIstYrCysAsnValLeuCysGlyGluArgGlu 100
317 ACCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 366
101 GluAlaArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgTh 117
367 GAGGACAGGGCTTGGCCACGCCACCCACACCCGCTGCTGCTGCTG 416
117 rGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysProP 134
417 CGGCTTCTTTCGCGCACGCTGCTTCTGCTGCTGCTGCTGCTGCT 466
134 roGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnTrpGlnCys 150
467 CTGGTCCGCGCTGATGCCCCGCGGACCCGACGCCGAAGACAGCGAGTC 516
151 GluProCysProProGlyThrPheSerAlaSerSerSerSerSerGlu 167
517 CAGCGCTGCCCCAGGACCTTCTCAGCCAGGAGCGCTCCAGCTCAGAGA 566
167 nCysGlnProHisArgAsnGlyThrAlaLeuGlyLeuAlaLeuAsnValP 184
567 GTCCGAGGCCACCGCACTGACGGCCCTGCGGCTGCGCTGCTCAATGTC 616
184 roGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPhePro 200
617 CAGGCTTCTTCTCCATGACACCTGTGACACAGCTGCTGCTGCTGCT 666
201 LeuSerThrArgValProGlyAlaGluGluCysGluArgAlaValIleAs 217
667 CTGAGGACAGGGTACAGAGACTGAGAGTGAAGTGAAGTGAAGTGA 716
217 pPheValAlaPheGlnAspIleSerIleLeuValArgLeuGluAlaLeuG 234
717 CTTTGGCTTTCAGAGACTCTCCATCAGAGAGCTGCAAGGCGCTCTTC 766
234 lnaAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGlyArg 250
767 AGGCGCTCGAGGCCCGGAGGAGGCTGGGCTGCGACACCAAGGCGGCGCC 816
251 AlaAlaLeuGluLeuValLeuArgArgArgLeuThrGluLeuLeuGlyAl 267
817 GGGCGCTTGCAGCTGAAGCTCGTGGGCGCTCAGGAGAGCTCTCTGGGG 866

```

```

267 aglnAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAla 284
867 GCAGAGCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 916
284 rGmetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 300
917 GGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCTCCGTGG 966

seq_name: /SIDSL/gcgdata/geneseq/geneseqn/AA2000.DAT:AAA53802
seq_documentation_block:
ID AAA53802 standard; CDNA; 1066 BP.
XX
AC AAA53802;
XX
DT 19-DEC-2000 (first entry)
XX
DE M68 TNF receptor related protein coding sequence.
XX
KW M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
KW receptor; immune response; cell differentiation; ligand; cancer;
KW bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
KW Grave's disease; idiopathic myxedema; autoimmune diabetes;
KW thrombotic thrombocytopenic purpura; multiple sclerosis;
KW liver diseases; autoimmune gastritis; ulcerative colitis;
KW glomerulonephritis; pulmonary fibrosis; heart failure;
KW atherosclerosis; aplastic anaemia; myelodysplastic syndromes;
KW osteoporosis; Alzheimer's disease; Parkinson's disease; stroke;
KW myocardial infarction; human; ds.
XX
OS Homo sapiens.
XX
FH key
FT location/Qualifiers
FT CDS 53..955
FT /tag= a
FT /product= M68 polypeptide
XX
XX WC0200046247-A1.
XX
PD 10-AUG-2000.
XX
PE 04-FEB-2000; 2000WO-US03037.
XX
PR 05-FEB-1999; 99US-0118902.
XX
PR 20-DEC-1999; 99US-0127254.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Bal C;
XX
DR WPI: 2000-506066/45.
XX
DR P-PSDB; AAY97246.
XX
PT Isolated human M68 nucleic acids and proteins which are part of the
PT tumour necrosis factor receptor (TNFR) family, useful for identifying
PT modulators that may be used to treat various diseases e.g. cancer,
PT osteoporosis, Alzheimer's disease
XX
PS Claim 21: Page 73-75; 80pp: English.
XX
XX The M68 protein is a member of a family of proteins which have
XX roles in immune responses, cell death, cell proliferation and
XX stimulation of cell differentiation. M68 lacks a transmembrane domain
XX and is a secreted factor suggesting that it functions as a natural
XX inhibitor for its ligand. The altered expression pattern of M68 in a
XX multitude of tissues suggests that M68 may play a role in cancer by
XX binding to its ligand and blocking apoptotic cell death induced by
XX such a ligand. This anti-apoptotic role of M68 suggests that
XX modulators of M68 will be useful in treatment of apoptosis-related
XX diseases such as various forms of cancer and various bone disorders.
XX M68 nucleic acids and proteins are therefore useful for treating
XX conditions involving atypical apoptosis and for identifying
XX modulators of M68. Modulators of M68 are useful for treatment of

```







CC prostate tumour tissue. For a number of disorders of these cells, CC particularly of the immune system, substantially altered (whether increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta polypeptides, nucleic acids and antibodies are claimed to be useful in the diagnosis of such disorders. Mutations of the TNFR-6 alpha and CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are CC claimed to be useful for identifying ligands which may be useful in the treatment of apoptosis related disorders.

XX Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

#### alignment\_scores:

Quality: 1634.00 Length: 300  
Ratio: 5.447 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

#### alignment\_block:

us-09-006-352-2 x AAV39085 ..

Align seg 1/1 to: AAV39085 from: 1 to: 1077

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1 MetATGAlaLeuGluGlyProGlyLeuSerLeuLeuValLeuAl 17
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17 AleuProAlaLeuLeuProValProAlaValArgGlyValAlaGluThrP 34
75 GCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 124
34 roThrTyProTrpArgAspAlaGluThrGlyGluArgLeuValAlaGlyAla 50
125 CCACCTACCCCTGGCGGAGCCAGACAGGAGGAGCGCTGTGTGTGTGCTG 174
51 GlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerPr 67
175 CAGTGTCCCGCCAGGACCTTGTGTGACGCGCGCTGTGCGCGAGACGCCC 224
67 oThrThrCysGlyProCysProProArgHisTyrThrGlnPheTyrPasnT 84
225 CAGAGCTGTGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 274
84 yTrpLeuAlaArgCysArgTyrCysAsnValLeuGlyGluArgGluGlu 100
275 ACCTGGAGGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 324
101 GlnAlaArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgTh 117
325 GAGGACAGGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 374
117 rGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysProP 134
375 CGGCTTCTTGTGCGACGCTGTGTCTGTGTGTGAGACAGATGATGTCAC 424
134 roGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCys 150
425 CTGGTCCCGCGGTGATTCCTCCCGGACCCCGACGACCAACGACGATGTC 474
151 GlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGlnG 167
475 CAGCGCTGTGCGCCCGAGGACCTTCTCAGCCACGACGCTCCAGCTCAGAGA 524
167 nCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValP 184
525 GTGGCAGGCGCCACGCACTGTACAGCGCTGTGCTGTGCTGTGCTGTGCTG 574
184 roGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPhePro 200
575 CAGGCTTCTTCCCTCCATGACACCTGTGTGACAGCTGTGCTGTGCTGTGCT 624
201 LeuSerThrArgValProGlyAlaGluGluCysGluArgAlaValIleAs 217
|||||

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```

625 CTCAGCACGAGGTACACGAGCTGAGGAGTGTGAGCGTCCCTCATCGA 674
217 pPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArgLeuGlu 234
675 CTGTGTGCTTGTCCAGAGACATCTCCATCAAGAGCTGTGACGCGCTGTG 724
234 IlnAlaLeuGluAlaProGluGluTyrProGlyProThrProArgAlaGlyArg 250
775 AGGCTTGTGAGCGCCCGGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 774
251 AlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrLeuLeuGluVal 267
775 GCGGCTTGTGACGCTGAACCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 824
267 aGlnAspGlyAlaLeuLeuValArgLeuGlnAlaLeuArgValAlaA 284
825 GCAAGACGAGGCGCTGTGTGTGCTGTGTGTGCTGTGTGTGCTGTGTGTG 874
284 rGlnMetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 300
875 GGATGCCCGGGCTGTGAGCGAGCGACGCTGTGTGAGCGCTGTGTGTGCTG 924

seq_name: /STD1/gcdata/geneseq/geneseqn/AA2000.DAT:AAA37772
seq_documentation_block:
ID AAA37772 standard: DNA, 1077 BP.
AC AAA37772;
DT 04-DEC-2000 (first entry)
DE Human tumour necrosis factor receptor-6 alpha coding sequence.
XX
XX Human: Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;
KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;
KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;
KW pre-matutally macular degeneration; allergy; inflammation; tissue damage;
KW thyroid associated ophthalmopathy; cell damage; parasitic infection;
KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;
KW neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;
KW psoriasis; septic shock; ulcerative colitis; therapy; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 25..927 /tag=a
XX FT /product= TNFR-6alpha
XX
XX WO2000052028-A1.
XX
XX 08-SEP-2000.
XX
XX 03-MAR-2000; 2000WO-US05686.
XX
XX 04-MAR-1999; 99US-0121774.
XX 12-MAR-1999; 99US-0124092.
XX 27-APR-1999; 99US-0131279.
XX 30-APR-1999; 99US-0131964.
XX 02-AUG-1999; 99US-0146371.
XX 01-DEC-1999; 99US-0168235.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Gentz RL, NI J, Bpner R, Yu G, Ruben SM, Feng P;
XX
XX MPI: 2000-572174/53.
XX P-PSDB: AAV90357.
XX
XX Nucleic acids encoding human tumour necrosis factor receptor (TNFR)
XX proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.
XX Alzheimer's disease, osteoporosis and graft rejection -

```



XX Claim 2: Fig 1: 332pp; English.  
PS  
XX  
CC This sequence encodes the human tumour necrosis factor receptor 6  
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA  
CC and protein sequences can be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate TNFR expression. The  
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against  
CC them may be used for the treatment of a range of conditions such as  
CC disorders associated with neovascularisation (especially ocular  
CC neovascularisation) (such as solid tumours and malignancies (e.g.  
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy  
CC and pre-maturity macular degeneration), allergies, inflammation,  
CC thyroid associated ophthalmopathy tissue/cell damage, wounds, microbial  
CC and parasitic infections, bone disease (e.g. osteoporosis),  
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),  
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune  
CC disorders (e.g. graft rejection), rheumatism, liver disease,  
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative  
CC colitis.  
XX  
SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other:

alignment\_scores:                   Quality: 1634.00                   Length: 300  
                                  Ratio: 5.447                   Gaps: 0  
Percent Similarity: 100.000       Percent Identity: 100.000

alignment\_block:

US-09-006-352-2 x AAA37772 ..

Align seg 1/1 to: AAA37772 from: 1 to: 1077

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25 ATGAGGCGCTGGAGGGCCAGGCGCTGCTGCTGCTGCTGGTGGC 74  
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17 AlaProAlaLeuLeuProValProAlaValArgGlyValAlaGluThrP 34  
  |||||  
75 GCGCGCGCGCTGCTGCGCGGTGCGGTGACCGGAGTGGCAGAAACAC 124  
  |||||  
34 roThrTyProTrPARgAspAlaGluThrGlyLuarGleuValCysAla 50  
  |||||  
125 CCACCTCCACCTGGCGCGGAGCAGACAGAGGAGCGCTGCTGGCGCC 174  
  |||||  
51 GluCysProProGlyThrPheValGlnArgProCysArgArgAspSerPr 67  
  |||||  
175 CAGTGGCCCCCAGGACACCTTTGTGACGGCGCGTGGCCGAGACAGCCC 224  
  |||||  
67 ofHrThrCysGlyProCysProProArgHnIsTyTrThGlnPheTrpAsnT 84  
  |||||  
225 CAGGAGCTGTGGCCCGTGTCCACCGCCGACACGAGTTCGGAAGT 274  
  |||||  
84 yrlLeuGluArgCysArgTyTrCysAsnValLeuCysGlyLuarGluGlu 100  
  |||||  
275 ACCTGAGAGCGCTGGCGCTACTGCAACGCTCTGCGGGAGCGAGAGAG 324  
  |||||  
101 GluAlaArgAlaCysHnIsAlaThrHnIsAsnArgAlaCysArgCysArgTh 117  
  |||||  
325 GAGGACAGGGGCTTGGCCAGCCACCAACCGTGGCCGCGCGCCGAC 374  
  |||||  
117 rGlyPhePheAlaHnIsAlaGlyPheCysLeuGluHnIsAlaSerCysProp 134  
  |||||  
375 CGGCTTCTTTCGCGCAGCGCTGTCTTCTGTTGAGACAGCAGTCTGTCAC 424  
  |||||  
134 roGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCys 150  
  |||||  
425 CTGGTGGCGGCGGATGATGCCCCGGGACCCCGAGCCAGAACAGCAGTGGC 474  
  |||||  
151 GlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlu 167  
  |||||  
475 CAGCGGTGGCCCCCAGGACACCTTCTCAGCCAGAGCTCCAGTCCAGAGCA 524

167 nCysGlnProHnIsArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValP 184  
  |||||  
525 GTGGCACCCCGACCGCAACTGACAGCGCGCTGGGCTGCTGCAATGTGC 574  
  |||||  
184 roGlySerSerSerHnIsAspThrLeuCysThrSerCysThrGlyPhePro 200  
  |||||  
575 CAGCGCTTCTTCCCATGACACCTGTGACACACCTGAGTGGCTTCC 624  
  |||||  
201 LeuSerThrArgValProGlyAlaGluGluCysGluArgAlaValIleAs 217  
  |||||  
625 CTACGACACAGGTTACCAAGAGCTGAGAGGTGTAGCGTCCGTCATCGA 674  
  |||||  
217 pPheValAlaPheGlnAspIleSerIleTyArgLeuGlnArgLeuLeuG 234  
  |||||  
675 CTTTGTCGCTTTCAGACACATCTCCATCAGAGGCTGACCGCTGCTGC 724  
  |||||  
234 lAlaLeuGluAlaPProGlyGlyTrpGlyProThrProArgAlaGlyArg 250  
  |||||  
725 AGGCGCTCGAGGCGCCCGAGGCGGTGGGTCCGACACCAAGGCGGCGCG 774  
  |||||  
251 AlAlaLeuGluLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAl 267  
  |||||  
775 GCGGCTTGGAGCTGAAGCTGCGTGGCGCTCAGGAGCTCTCGTGGGGC 824  
  |||||  
267 aGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAla 284  
  |||||  
825 GCAGGAGGCGGCGCTGCTGCTGCGCTGCTGACAGCGCTGCGCTGGSCA 874  
  |||||  
284 rGmetProGlyLeuGluArgSerValArgGluArgPheLeuProValHnIs 300  
  |||||  
875 GGATGCCCGGGGCTGGAGCGGAGCGCTCCGTGAGCGCTTCTCCGTGTCAC 924

seq\_name: /sids1/gcgcdata/geneseq/geneseqn/NA1999.DAT.AAA32744

seq\_documentation\_block:

ID AAA32744 standard; DNA; 1114 BP.

XX AAA32744;

XX 24-JUN-1999 (first entry)

XX Human DCr3 polypeptide encoding DNA.

XX DCr3 polypeptide; tumour necrosis factor receptor; TNFR; Fas ligand;

XX apoptosis; T cell mediated immune response; allergy; asthma; cancer;

XX rheumatoid arthritis; Crohn's disease; guest vs. host disease; human;

XX gene therapy; ss.

XX Homo sapiens.

XX W09914330-A1.

XX 25-MAR-1999.

XX 18-SEP-1998; 98WO-US19661.

XX 30-JUL-1998; 98US-0094640.

XX 18-SEP-1997; 97US-0059288.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Botstein D, Dodge KH, Goddard A, Gurney AL,

XX Kim KJ, Lawrence DA, Pittl R, Roy MA, Tumas DB;

XX Wood WT;

XX WPI; 1999-244032/20.

XX P-PSDB; AAY06817.

XX DCr3 polypeptide related to tumor necrosis factor receptor

XX Examples; Fig 2; 88pp; English.



















```

|||||
601 GTGCGAGCCGCCACGACCTGACGGCCGTGGCGCTGGCCCTCAATGTC 650
184 rogliserSerSerHisAspThrLeucysTherSerCysThrGlyPhePro 200
651 CAGGCTCTTCCTCCATGACACCTGTGACACAGCTGACATGCTTCCCC 700
201 LeuSerThrArgValProGlyAlaGluGlyCysGluArgAlaValIleAs 217
701 CTGAGCACCAGGATACAGAGAGCTGAGAGTGTGAGCGTCCGTCATGCA 750
217 pPheValAlaPheGlnAspIleSerIleLysArgIleGlnArgIleLeuG 234
751 CTTTGTGGCTTCCAGAGCATCTCCATCAAGAGCGTGCAGCGCTCTGTC 800
234 lAlaLeuGlnAlaProGlnGlyTrpGlyProThrProArgAlaGlyArg 250
801 AGGCGCTCGAGGCCCGGAGGGCTGGGTCGACACCAAGCGCGGCCCC 850
251 AlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAla 267
851 GCGGCTTGCACCTGACCTGAGCTGGGTGGGTGCTGAGAGTCTGTGGGGC 900
267 aglnaPglYAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAla 284
901 GCGAGGAGGGGGCGCTGCTGTGGCGCTGCAAGCGCTGGCGTGCCCA 950
284 rGMeTrProGlyLeuGlnArgSerValArgGlnArgPheLeuProValHis 300
951 GGATGGCCCGGCTGAGCGAGCGCTCGTGAGCGCTTCCCTCCCTGTGACC 1000

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seq_documentation_block:
ID AAC84421 standard; cDNA; 1114 BP.
XX AAC84421;
XX
XX 02-APR-2001 (first entry)
XX
XX Human PRO212 polypeptide encoding cDNA.
XX
XX PRO212; PRO212; PRO212; neoplastic; cell growth; tumour; cancer;
XX breast; ovarian; renal; colorectal; uterine; prostate; lung; melanoma;
XX central nervous system; leukemia; antitumor; cytostatic; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 101..1003
XX FT /*tag= a
XX FT /*product= "PRO212"
XX FT sig_peptide 101..169
XX FT /*tag= b
XX FT mat_peptide 170..1111
XX FT /*tag= c
XX
XX WO200075316-A1.
XX
XX 14-DEC-2000.
XX
XX 20-DEC-1999; 99WO-US30911.
XX
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 07-JUL-1999; 99US-0143048.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 30-NOV-1999; 99WO-US28313.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Goddard A, Gurney AL, Hillan K, Napier M, Wood WT;

```

```

XX
XX WPI: 2001-050025/06.
DR P-PSDB: AAB48161.
XX
XX Composition for inhibiting neoplastic cell growth and treating a tumor
XX or cancer, comprises novel PRO212, PRO326, PRO1016 polypeptides or
XX agonists of them
XX
XX Claim 19; Fig 1; 116pp; English.
XX
XX The invention provides PRO212, PRO326 or PRO1016 polypeptides that can be
XX used for the inhibition of neoplastic cell growth and for treating
XX tumours. The PRO polypeptides can be expressed by standard recombinant
XX methodology. The PRO polypeptides or their agonists are useful for
XX inhibition of neoplastic cell growth and for treating tumours, cancers
XX such as breast, ovarian, renal, colorectal, uterine, prostate, lung, the
XX bladder or central nervous system cancers or melanoma and leukemia. The
XX present sequence represents the cDNA encoding the human PRO212
XX polypeptide.
XX
XX Sequence 1114 BP; 188 A; 379 C; 356 G; 191 T; 0 other:
XX
XX
XX alignment_scores:
XX      Quality: 1634.00      Length: 300
XX      Ratio: 5.447      Gaps: 0
XX Percent Similarity: 100.000      Percent Identity: 100.000
XX
XX alignment_block:
XX US-09-006-352-2 x AAC84421 ..
XX
XX Align seq 1/1 to: AAC84421 from: 1 to: 1114
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XX |||||
XX 151 GTCGCTGCGCTGCTGCGGCTGCGGCTGTACGGAGTGGCAGAAACAC 200
XX
XX 34 norPTrpProTrpArgAspAlaGluThrGlyGlnArgLeuValCysAla 50
XX |||||
XX 201 CCACTACCCCTGCGCGGAGCAGAGACAGAGGAGCGCGCTGCTGCGCC 250
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ID AAW63622 standard; Protein; 300 AA.

AC AAW63622;

XX 26-OCT-1998 (first entry)  
XX  
DE Human tumour necrosis factor receptor-6 alpha protein.  
KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 beta  
KW endothelial cells; keratinocytes; normal prostate; apoptosis;  
KW prostate tumour tissue.  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..30  
FT Protein 31..300  
FT /note= "TNFR-6 alpha"  
FT 31..282  
FT Region /note= "Soluble extracellular domain"

PN WO9803694-A2.  
PD 16-JUL-1998.  
PI 13-JAN-1998; 98WO-US00153.  
PF  
PR 14-JAN-1997; 97US-0035496.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Ebnner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;  
DR WPL: 1998-399142/34.  
DR N-PDB: AAV39085.  
XX

PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in  
PT the diagnosis of immune system-related disorder(s)  
XX

PS Claim 20; Fig 1; 91pp; English.

CC The present sequence represents the human tumour necrosis factor  
CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides  
CC for the TNFR-6 beta protein (AAW63623). TNFR-6 alpha and TNFR-6 beta  
CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs  
CC are expressed in endothelial cells, keratinocytes, normal prostate and  
CC prostatic tumour tissue. For a number of disorders of these cells,  
CC particularly of the immune system, substantially altered (whether  
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene  
CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta  
CC polypeptides, nucleic acids and antibodies are claimed to be useful in  
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and  
CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are  
CC also claimed to be useful for identifying ligands which may be useful  
CC in the treatment of apoptosis related disorders.  
XX

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Percent Similarity: 100.000 Percent Identity: 100.000

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1 leuProAlaleLeuIeuProValIProAlaValAtArgGIyValAlaIGluTrpP 34



































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625 CTCACACACAGGCTACAGAGCTGAGAGTGAAGTGAAGCGTGCCTATGCA 674
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 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human PRO212 protein sequence SEO ID NO:2.  
 XX

KM Human: tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 KW proliferation; tumourigenesis; identification; cancer; cytostatic;  
 KW neotropic; neuroprotective; antiinflammatory; immunosuppressive;  
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
 KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
 KW hypothalamic disorder; glandular disorder; macropnagal disorder;  
 KW epithelial disorder; stromal disorder; blastocoelec disorder;  
 KW inflammatory disorder; immunologic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN M0200053755-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PE 06-JAN-2000; 2000MO-US00376.  
 XX  
 PR 08-MAR-1999; 99MO-US05028.  
 PR 02-JUN-1999; 99MO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 05-JAN-2000; 2000MO-US00219.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
 PI Watanabe CK, Wood WI;  
 XX  
 DR WPI: 2000-572270/53.  
 DR N-PSDB; AAC58367.  
 XX  
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 FT treatment, diagnosis and prevention of cancer -  
 XX  
 PS  
 PS  
 PS Claim 61: Fig 2; 286bp; English.

CC The present invention describes an isolated antibody that binds to  
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO355,  
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
 CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,  
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
 CC growth. The PRO polypeptides and nucleotides are useful in the  
 CC treatment, diagnosis and prevention of cancer. The antibodies and other  
 CC anti-tumour compounds may be used to treat various conditions, including  
 CC those characterised by overexpression and/or activation of the amplified  
 CC PRO genes. Exemplary conditions or disorders to be treated with such  
 CC antibodies and other compounds include benign or malignant tumours  
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
 CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),  
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,  
 CC glial, astrocytal, hypothalamic and other glandular, macropnagal,  
 CC epithelial, stromal and blastocoelec disorders, and inflammatory,  
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
 CC primers and hybridisation probes used in the isolation of the human PRO  
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
 CC PRO polynucleotide and protein sequences given in the exemplification of  
 CC the present invention.  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2001, 09:41:14 ; Search time 1944.49 Seconds  
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Maximum DB seq length: 200000000

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Maximum Match 100%

Listing first 45 summaries

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3	1032.8	95.9	4228	85 AB029011	AB029011 Homo sapi
4	1019	94.6	1048	89 AF217794	AF217794 Homo sapi
5	1019	94.6	1114	9 AX055373	AX055373 Sequence
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[illegible]

## ALIGNMENTS

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ORGANISM    human.
REFERENCE   1
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE       Duesteroeltz,A., Lauber,J., Mewes,H.W., Well,B. and Wiemann,S.
JOURNAL     Direct Submission
COMMENT     Submitted (15-FEB-2000) MIPS. Am Klopferstr. 18a, D-82152
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            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
            sequenced by Olagen (Hilden/Germany) within the CDNA sequencing
            consortium of the German Genome Project.
            This clone (DKFZP434O0510) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://www.mips.biochem.mpg.de/proj/cDNA/.
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AUTHORS Bai, C.  
TITLE Direct Submission  
JOURNAL Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,  
Summeytown Pike, West Point, PA 19403, USA  
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ACCESSION AX055373  
VERSION AX055373.1 GI:12228659  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1114)  
AUTHORS Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,  
Turney, D., Watanabe, C.K. and Wood, W.I.  
COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED  
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TITLE 1 JOURNAL  
patent: WO 0073452-A 3 07-DEC-2000;  
location/Qualifiers  
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DB 137 TGCCTGGTGTGGCGGCTTCTTGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 196  
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REFERENCE 1 (bases 1 to 1114)  
Pilti, R.M., Marsters, S.A., Lawrence, D.A., Roy, M., Kischkel, F.C.,  
Dowd, P., Huang, A., Donahue, C.J., Sherwood, S.W., Baldwin, D.T.,  
Godowski, P.J., Wood, W.I., Gurney, A.L., Hillan, K.J., Cohen, R.L.,  
Goddard, A.D., Botstein, D. and Ashkenazi, A.  
Genomic amplification of a decoy receptor for Fas ligand in lung  
and colon cancer  
Nature 396 (6712), 699-703 (1998)  
JOURNAL MEDLINE 99087326  
2 (bases 1 to 1114)  
Pilti, R.M., Marsters, S.A., Lawrence, D.A., Roy, M., Kischkel, F.C.,  
Dowd, P., Huang, A., Donahue, C.J., Sherwood, S.W., Baldwin, D.T.,  
Godowski, P.J., Wood, W.I., Gurney, A.L., Hillan, K.J., Cohen, R.L.,  
Goddard, A.D., Botstein, D. and Ashkenazi, A.  
Direct Submission  
TITLE Submitted (04-NOV-1998) Molecular Oncology, Genentech, 1 DNA Way,  
JOURNAL San Francisco, CA 94080, USA  
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BASE COUNT 188 a 379 c 356 g 191 t  
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Best Local Similarity 100.0%; Pred. No. 1.3e-180;  
Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 121 acaccac 180  
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LOCUS AX082868 Sequence 1 from Patent WO0110908.  
DEFINITION AX082868  
ACCESSION AX082868.1 GI:13184802  
VERSION



KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1055)

AUTHORS Hsu, H.

JOURNAL Nfya, a member of the tnfr-receptor supergene family  
Patent: WO 0110908-A 1 15-FEB-2001;

FEATURES

source

Location/Qualifiers

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DEFINITION AF217793  
ACCESSION AF217793.1 GI:5969260

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota;

Mammalia;

Eutheria;

Primates;

Catarrhini;

Homnidae;

Homo.

1 (bases 1 to 1428)

REFERENCE

AUTHORS

Bai, C., Connolly, B., Metzger, M. L., Hilliard, C. A., Liu, X.,

Sandley, Y., Soderman, A., Galloway, S. M., Liu, Q., Austin, C. P., and

Overexpression of M68/DCR3 in human gastrointestinal tract tumors

Independent of gene amplification and its location in a four-gene

cluster

Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Bai, C.

Direct Submission

Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,

Summeytown Pike, West Point, PA 19403, USA

Location/Qualifiers

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KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS 1 (bases 1 to 936)  
TITLE Altkinson, P. R., Tian, Y., and Mitcher, D. R.  
JOURNAL Flint analog compounds and formulations thereof  
Patent: WO 0118202-A 3 15-MAR-2001;  
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complete cds.  
ACCESSION AF134240  
VERSION AF134240.1 GI:4768938  
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SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 903)  
AUTHORS Yu, K.Y., Kwon, B., Ni, J., Zhai, Y., Ebner, R., and Kwon, B. S.  
TITLE A newly identified member of tumor necrosis factor receptor  
superfamily (TR6) suppresses LIGCH-mediated apoptosis  
JOURNAL J. Biol. Chem. 274 (20), 13733-13736 (1999)  
MEDLINE 99253915  
REFERENCE 2 (bases 1 to 903)  
AUTHORS Kwon, B. S. and Yu, K. Y.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAR-1999) Micro/Immunol, Indiana University, 635  
Barnhill Drive, Indianapolis, IN 46202, USA  
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source location/Qualifiers  
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DB 341 GCTCTCCCTCTCCAGCAAGACCATGAGGGCGCTGAGGGCGCAGGCCCTGCTGCTG 400  
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QY 61 tgcctggtgttgagcgctgcctgcctgcctgcctgcctgctgacgcgagtgagcaaa 120  
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DB 401 TGGCTGCTGTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 460  
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REFERENCE	266 (bases 1 to 114793)		
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REFERENCE	289 (bases 1 to 114793)		
REFERENCE	290 (bases 1 to 114793)		
REFERENCE	291 (bases 1 to 114793)		
REFERENCE	292		







Mon Nov 5 08:22:32 2001

us-09-006-352-1.rge

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OM nucleic - nucleic search, using sw model

Run on: October 31, 2001, 09:41:15 ; Search time 290.92 Seconds

(without alignments)  
2324.522 Million cell updates/sec

Title: US-09-006-352-1

Perfect score: 1077

Sequence: 1 gctccctgctccgacgaag.....aaaaaaaaaaaaaaaa 1077

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_0601.\*  
1: /SIDSI/gcgdata/geneseq/geneseqn/NA1980.DAT.\*  
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4: /SIDSI/gcgdata/geneseq/geneseqn/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseqn/NA1984.DAT.\*  
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21: /SIDSI/gcgdata/geneseq/geneseqn/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseqn/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1077	100.0	1077	19	AAV39085 Human tumour necro
2	1077	100.0	1077	21	AAA37772 Human tumour necro
3	1077	100.0	1164	19	AAV07654 Nucleotide sequenc
4	1059.8	98.4	1137	21	AAZ92404 CDNA encoding huma
5	1059	98.3	1168	20	AAZ09998 Human Lung TNF-rec
6	1030	95.6	1347	21	AAZ63764 Human soluble TNF
7	1028.8	95.5	1462	20	AAZ76052 Mammalian tumour r
8	1019	94.6	1066	21	AAZ53802 M68 TNF receptor r
9	1019	94.6	1114	21	AAZ58367 Human PRO212 nucle
10	1019	94.6	1114	21	AAZ58581 Human PRO212 prote
11	1019	94.6	1114	21	AAZ7537 Human PRO212 CDNA

12	1019	94.6	1114	22	AAZ84421 Human PRO212 polyp
13	1019	94.6	1114	22	AAZ91462 Human PRO212 CDNA
14	1019	94.6	1205	20	AAZ07226 Human tumour necro
15	1018	94.5	1114	20	AAZ32744 Human DCR3 polypep
16	1013	94.1	1055	22	AAZ62705 Human NTR3 nucleot
17	1002.8	93.1	1428	21	AAZ53801 M68 TNF receptor r
18	934.4	86.6	936	20	AAZ25376 Human FLINT #2 nuc
19	932.8	86.6	936	21	AAZ8731 Human FAS ligand 1
20	932.8	86.6	936	21	AAZ51076 Human FLINT coding
21	932.8	86.6	936	22	AAZ7696 Human FLINT native
22	903	83.8	903	20	AAZ23300 Orphan receptor (H
23	900	83.6	900	20	AAZ25375 Human FLINT #1 nuc
24	900	83.6	900	21	AAZ53208 Human Fas ligand 1
25	900	83.6	900	21	AAZ51075 Human FLINT coding
26	823.4	76.5	825	20	AAZ25378 Human FLINT #2 nu
27	823.4	76.5	825	21	AAZ51078 Human mature FLINT
28	813	75.5	813	20	AAZ25377 Human mature FLINT
29	813	75.5	813	21	AAZ75999 Human mFLINT #1 nu
30	813	75.5	813	21	AAZ8730 Human FAS ligand 1
31	813	75.5	813	21	AAZ51077 Mature human FLINT
32	797.6	74.1	900	21	AAZ53209 Monkey Fas ligand
33	755.2	70.1	899	20	AAZ89503 DNA encoding a hum
34	742	68.9	767	20	AAZ23419 Human APO6 DNA. H
35	644.4	59.8	1859	21	AAZ63765 Human soluble TNF
36	498.4	46.3	1667	19	AAZ39086 Human tumour necro
37	498.4	46.3	1667	21	AAZ3773 Human tumour necro
38	492	45.7	7720	21	AAZ53800 Genomic DNA encodi
39	473.4	44.0	491	20	AAZ32745 Human DCR3 EST seq
40	459	42.6	459	20	AAZ84621 Human TNFR superfa
41	459	42.6	459	21	AAZ63757 Human TNFR soluble
42	394.4	36.6	397	20	AAZ07227 Human tumour necro
43	305.2	28.3	497	19	AAZ39094 HEIDI6R DNA seque
44	305.2	28.3	497	21	AAZ3774 Human tumour necro
45	245.2	22.8	271	20	AAZ32747 Human DCR3 EST seq

#### ALIGNMENTS

RESULT 1	
ID	AAV39085 standard; CDNA; 1077 BP.
AC	AAV39085;
XX	
DT	.26-OCT-1998 (first entry)
XX	
DE	Human tumour necrosis factor receptor-6 alpha cDNA.
XX	
KW	Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW	endothelial cells; keratinocytes; normal prostate; apoptosis;
KW	prostate tumour tissue; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	25..927
FT	Location/Qualifiers
FT	/*tag= a
FT	/product= "TNFR-6 alpha protein"
FT	25..114
FT	/*tag= b
FT	115..924
FT	/*tag= c
XX	
PN	W09830694-A2.
XX	
PD	16-JUL-1998.
XX	
PF	13-JAN-1998; 98WO-US00153.
XX	
PR	14-JAN-1997; 97US-0035496.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.







PA (HUMA-) HUMAN GENOME SCI INC.  
XX Gentz RL, Ni J, Ebner R, Yu G, Ruben SM, Feng P;  
PI  
XX  
XX  
DR MPI: 2000-572174/53.  
XX  
XX P-PSDB: AAY90357.  
PT Nucleic acids encoding human tumour necrosis factor receptor (TNFR)  
PT Proteins TNFR-galpa and TNFR-6beta, useful for treating e.g.  
PT Alzheimer's disease, osteoporosis and graft rejection  
XX  
XX  
PS Claim 2: Fig 1: 332pp: English.  
XX  
XX This sequence encodes the human tumour necrosis factor receptor 6  
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA  
CC and protein sequences can be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate TNFR expression. The  
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against  
CC them may be used for the treatment of a range of conditions such as  
CC disorders associated with neovascularisation (especially ocular  
CC neovascularisation) (such as solid tumours and malignancies (e.g.  
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy  
CC and pre-maturity macular degeneration), allergies, inflammation,  
CC thyroid associated ophthalmopathy tissue/cell damage, wounds, microbial  
CC and parasitic infections, bone disease (e.g. osteoporosis),  
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),  
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune  
CC disorders (e.g. graft rejection), rheumatism, liver disease,  
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative  
CC colitis.  
XX  
XX  
SQ Sequence 1077 BP: 196 A; 360 C; 326 G; 195 T; 0 other;  
  
Query Match 100.0%; Score 1077; DB 21; Length 1077;  
Best Local Similarity 100.0%; Pred. No. 2.3e-190;  
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 541 aactgcacggccctggcctggccctcaatgtgcacagctcttccctccatgacacctg 600  
DB 541 aactgcacggccctggcctggccctcaatgtgcacagctcttccctccatgacacctg 600  
QY 601 tgcacacagctgcactgtgtccctccctccacacacagaggtaccagagcttgagatgtgag 660  
DB 601 tgcacacagctgcactgtgtccctccctccacacacagaggtaccagagcttgagatgtgag 660  
QY 661 cgtgcacatcagcttctgtgtcttcacagacatcccatcaagagctgcacagctg 720  
DB 661 cgtgcacatcagcttctgtgtcttcacagacatcccatcaagagctgcacagctg 720  
QY 721 ctgcagccctcgaagcccgccgagagctgggtlccgacacacacagagcgccgagcc 780  
DB 721 ctgcagccctcgaagcccgccgagagctgggtlccgacacacacagagcgccgagcc 780  
QY 781 ttgagctgaagctgcgtgcgtgcgtgcacagagctccttgaggcgacagagcgctg 840  
DB 781 ttgagctgaagctgcgtgcgtgcgtgcacagagctccttgaggcgacagagcgctg 840  
QY 841 ctggtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtg 900  
DB 841 ctggtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtg 900  
QY 901 cgtgcagctctcctccctgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtg 960  
DB 901 cgtgcagctctcctccctgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtg 960  
QY 961 gcacccacattgcactgaagaagcttttttaataagaagaatgagtttctaag 1020  
DB 961 gcacccacattgcactgaagaagcttttttaataagaagaatgagtttctaag 1020  
QY 1021 ctatttttaagaagcttttctataaataaataaataaataaataaataaataa 1077  
DB 1021 ctatttttaagaagcttttctataaataaataaataaataaataaataaataa 1077

RESULT 3  
AAV07654  
ID AAV07654 standard; cDNA; 1164 BP.  
XX  
XX AAV07654;  
XX  
XX  
XX 02-DEC-1998 (first entry)  
XX  
XX  
XX Nucleotide sequence of tumour necrosis related receptor (TR4).  
XX  
XX Human; tumour necrosis related receptor; TR4; agonist; antagonist;  
KW Inhibition; chronic; acute; inflammation; arthritis; septicemia;  
KW autoimmune disease; transplant rejection; stroke; cancer;  
KW Alzheimer's disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX  
XX  
XX Key Location/Qualifiers  
FT CDS 111..1013  
FT /tag= a  
FT /product= "human TR4"  
XX  
XX EP861850-A1.  
XX  
XX 02-SEP-1998.  
XX  
XX 20-JAN-1998; 98EP-0300382.  
XX  
XX 04-FEB-1997; 97US-0794796.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX Emery J, Tan KB, Truneh A, Young PR;  
XX  
XX  
XX MPI: 1998-508248/44.



DR P-PSDB; AAM66102.  
 XX New DNA encoding tumour necrosis related receptor - used to treat  
 PT and prevent e.g. inflammation, arthritis, septicaemia, autoimmune  
 PT diseases, transplant rejection, infection, stroke, ischaemia, ARDS,  
 PS restenosis, AIDS, bone disorders and cancer  
 PS Claim 3: Fig 1: 21bp: English.  
 XX This is the nucleotide sequence of the human tumour necrosis related  
 CC receptor (TR4), used in the method of the invention. The TR4 protein  
 CC or its agonist can be used to treat a subject in need of enhanced  
 CC TR4 polypeptide activity. The antagonist is used to inhibit TR4  
 CC polypeptide activity. The active agents can be used for the  
 CC treatment and prevention of diseases such as chronic and acute  
 CC inflammation, arthritis, septicaemia, autoimmune diseases, transplant  
 CC rejection, stroke, cancer, Alzheimer's disease.  
 XX  
 SO Sequence 1164 BP; 206 A; 396 C; 355 G; 207 T; 0 other:

Query Match 100.0%: Score 1077; DB 19; Length 1164;  
 Best Local Similarity 100.0%: Pred No. 2, 3e-10;  
 Matches 1077; Conservative 0; Mismatches 0; Indels 0; Caps 0;

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 Db 87 gctctccctgctcagagacacatgagcgtgagagagccagcgtctgctctg 146  
 OY 61 tgcctggtgttgctgctgctgctgctgctgctgctgctgctgctgctg 120  
 Db 147 tgcctggtgttgctgctgctgctgctgctgctgctgctgctgctgctg 206  
 OY 121 aacacccactacccttgcgagagacagagagagagagagctgctgctgctg 180  
 Db 207 aacacccactacccttgcgagagacagagagagagagagctgctgctgctg 266  
 OY 181 ccccccagacatttgcagacgagcgtgctgctgctgctgctgctgctgctg 240  
 Db 267 ccccccagacatttgcagacgagcgtgctgctgctgctgctgctgctgctg 326  
 OY 241 tgcacacgagcactacacagcagcttctggaactctgagcgtgctgctgctg 300  
 Db 327 tgcacacgagcactacacagcagcttctggaactctgagcgtgctgctgctg 386  
 OY 301 gtccctcgcgagagcgtgagagagagagagagcgttgcacacgacacacgctg 360  
 Db 387 gtccctcgcgagagcgtgagagagagagagagcgttgcacacgacacacgctg 446  
 OY 361 tgcctggtgcgagcagcgttcttgcgacgctggttcttgcgttgcgttgcgtt 420  
 Db 447 tgcctggtgcgagcagcgttcttgcgacgctggttcttgcgttgcgttgcgtt 506  
 OY 421 ccaacctggtgcgagcgttcttgcgacgctggttcttgcgttgcgttgcgtt 480  
 Db 507 ccaacctggtgcgagcgttcttgcgacgctggttcttgcgttgcgttgcgtt 566  
 OY 481 tgcctcgcgagcagccttctcagcagcagctcagctcagctcagctcagctc 540  
 Db 567 tgcctcgcgagcagccttctcagcagcagctcagctcagctcagctcagctc 626  
 OY 541 aactgcagagccttgcgagcgttgcctcaatgtgcagagcttcttctcctcagac 600  
 Db 627 aactgcagagccttgcgagcgttgcctcaatgtgcagagcttcttctcctcagac 686  
 OY 601 tgcacagagctgacgtgcttccctcagacacagaggtaccagagcgtgagagtg 660  
 Db 687 tgcacagagctgacgtgcttccctcagacacagaggtaccagagcgtgagagtg 746  
 OY 661 cgtgcagcagcagcagcttgcgttctcagagacatctcagagagcgtcagagcgt 720  
 Db 747 cgtgcagcagcagcagcttgcgttctcagagacatctcagagagcgtcagagcgt 806

OY 721 ctgcagcctctcagagcctcccgagagcgtggtctcgcacaccaaagcgagcgcgcg 780  
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 OY 781 ttgcagctgaagctgctgctgcgcgtcagagctcctcgtgagcagagcagcgcgtg 840  
 Db 867 ttgcagctgaagctgctgctgcgcgtcagagctcctcgtgagcagagcagcgcgtg 926  
 OY 841 ctgctgcgctcgtcagagcgtcgcgtgcgcagagatgcccgagcgtgagcgcgtc 900  
 Db 927 ctgctgcgctcgtcagagcgtcgcgtgcgcagagatgcccgagcgtgagcgcgtc 986  
 OY 901 cgtgagcgtctcctcctcgtgcagctgacgtatccctcgttattatctacatctg 960  
 Db 987 cgtgagcgtctcctcctcgtgcagctgacgtatccctcgttattatctacatctg 1046  
 OY 961 gcacccacttgcagagagcgttcttcttaataagaaatgaggttcttaag 1020  
 Db 1047 gcacccacttgcagagagcgttcttcttaataagaaatgaggttcttaag 1106  
 OY 1021 ctatttttataagcttcttcttaataagaaatgaggttcttaag 1077  
 Db 1107 ctatttttataagcttcttcttaataagaaatgaggttcttaag 1163

RESULT 4  
 AAZ92404  
 ID AAZ92404 standard; CDNA: 1137 BP.

AAZ92404;  
 AC 05-JUN-2000 (first entry)

DE cDNA encoding human TNF receptor-like protein, HDTEA84.

KW TNF receptor family; tumour necrosis factor; HDTEA84; HSLJD37R;  
 KW Rank-like protein; RANKL; immune disorder; inflammation; allergy;  
 KW immunosuppressant; antiarthritis; antirheumatoid; antiinflammatory;  
 KW dermatological; antihypoid; ss.

OS Homo sapiens.

XX Key. Location/Qualifiers  
 FT CD5 99..1001  
 FT /tag= a  
 FT /product= "Human HDTEA84"

PN WO200001817-A2.

PD 13-JAN-2000.

PE 06-JUL-1999; 99WO-US12366.

XX 06-JUL-1998; 980S-0110938.

PR 13-JUL-1998; 980S-0114466.

PR 23-JUL-1998; 980S-0093897.

PR 12-AUG-1998; 980S-0132968.

PR 18-AUG-1998; 980S-0136214.

PR 11-SEP-1998; 980S-0099999.

XX (SCHE ) SCHERING CORP.

PI Bates EM, Lebeque SE, Murphy EE, Mattson JD, Gorman DM;  
 PI Hedrick JA, Wang L, Zlounik A, Murgolo NJ, Greene JR, Johnston JA;  
 PI Bazan JF, Mahony D, Lees EM;

XX WPI: 2000-171015/15.

DR P-PSDB; AAV77458.

XX New isolated mammalian genes, used to develop products for treating  
 PT e.g. immune, inflammatory or allergic abnormalities, cancers or  
 PT degenerative conditions -























CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,  
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
growth. The PRO polypeptides and nucleotides are useful in the  
CC treatment, diagnosis and prevention of cancer. The antibodies and other  
CC anti-tumour compounds may be used to treat various conditions, including  
CC those characterised by overexpression and/or activation of the amplified  
CC PRO genes. Exemplary conditions or disorders to be treated with such  
CC antibodies and other compounds include benign or malignant tumours  
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
CC leukemias, sarcomas, glioblastomas, and various head and neck tumours),  
CC glioma, astrocytoma, hypothalamic and other glandular, macrophagel,  
CC epithelial, stromal and blastocoele disorders, and inflammatory,  
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
CC primers and hybridisation probes used in the isolation of the human PRO  
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
CC PRO polynucleotide and protein sequences given in the exemplification of  
CC the present invention.  
XX  
SQ Sequence 1114 BP: 188 A: 379 C: 356 G: 191 T: 0 other:

Query Match 94.6%; Score 1019; DB 21; Length 1114;  
Best Local Similarity 100.0%; Pred. No. 1.2e-179;  
Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 77 gctctccctgctcagcaagacacgagcgctgagagggccagccctgctgctg 136  
OY 61 tgcctgtgtgtgagcctgctcctgctcctgctcctgctcctgctcctgctcctg 120  
DB 137 tgcctgtgtgtgagcctgctcctgctcctgctcctgctcctgctcctgctcctg 196  
OY 121 acacccac 180  
DB 197 acacccac 256  
OY 181 ccccccagcactctgtgcaagcgctgctcctgctcctgctcctgctcctgctcctg 240  
DB 257 ccccccagcactctgtgcaagcgctgctcctgctcctgctcctgctcctgctcctg 316  
OY 241 tgcacacgcgcac 300  
DB 317 tgcacacgcgcac 376  
OY 301 gtccctctgagagagcgtgagagagagagagagagagagagagagagagagagag 360  
DB 377 gtccctctgagagagcgtgagagagagagagagagagagagagagagagagagag 436  
OY 361 tgcagctgag 420  
DB 437 tgcagctgag 496  
OY 421 ccaactgtgtgctgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 480  
DB 497 ccaactgtgtgctgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 556  
OY 481 tgcacccagcagcactctcagcagcagcactcagcagcagcactcagcagcagcactc 540  
DB 557 tgcacccagcagcactctcagcagcagcactcagcagcagcactcagcagcagcactc 616  
OY 541 aactgacagcgccttgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 600  
DB 617 aactgacagcgccttgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 676  
OY 601 tgcacacagctgacgtgcttccctcagacacacagagagagagagagagagagagagag 660  
DB 677 tgcacacagctgacgtgcttccctcagacacacagagagagagagagagagagagagag 736

OY 661 cgtgcac 720  
DB 737 cgtgcac 796  
OY 721 ctgagagccctcagagcccccagagagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 780  
DB 797 ctgagagccctcagagcccccagagagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 856  
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DB 857 ttgacagctgaagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 916  
OY 841 ctggtgagcgtgctgagagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 900  
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DB 977 cgtgagagcgttccctcctgctgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 1036  
OY 961 gcacccacactgacacgagagcgttctttaaataagaagaatgaggttctttaa 1019  
DB 1037 gcacccacactgacacgagagcgttctttaaataagaagaatgaggttctttaa 1095

RESULT 10  
AAC58581  
ID AAC58581 standard; cDNA: 1114 BP.  
XX  
AC AAC58581;  
DT 29-JAN-2001 (first entry)  
XX  
XX Human PRO212 protein UNQ106 encoding cDNA SEQ ID NO:13.  
DE  
XX  
XX Human: immune related disease; diagnosis; anti-inflammatory; candidant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW hemostatic; antithyroid; antidiabetic; neotropic; neuroprotective;  
KW antianemic; hepatotropic; virucide; antiparasitic; antiallergic;  
KW antisthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW autoimmune thrombocytopenia; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease; SS.  
OS Homo sapiens.  
XX  
XX W0200053758-A2.  
FN 14-SEP-2000.  
FD  
XX  
XX 02-MAR-2000; 2000MO-US05841.  
FE  
XX  
XX 08-MAR-1999; 99MO-US05028.  
PR 10-MAR-1999; 99US-0123618.  
PR 12-MAR-1999; 99US-0123957.  
PR 23-MAR-1999; 99US-0125775.  
PR 12-APR-1999; 99US-0128849.  
PR 20-APR-1999; 99MO-US08615.  
PR 28-APR-1999; 99US-0131445.  
PR 04-MAY-1999; 99US-0132371.  
PR 14-MAY-1999; 99US-0134287.  
PR 23-JUN-1999; 99MO-US12252.  
PR 02-JUN-1999; 99MO-US141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99MO-US20111.















XX WO200073452-A2.  
XX  
XX  
PD 07-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-US15264.  
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PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144732.  
PR 20-JUL-1999; 99US-0144732.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28363.  
PR 09-DEC-1999; 99US-0170262.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 11-FEB-2000; 2000WO-US00376.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04342.  
PR 24-FEB-2000; 2000WO-US04414.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
PI Wood WI;  
XX  
XX WPI: 2001-025253/03.  
DR P-PSDB; AAB50903.  
XX  
XX  
XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
PT in the diagnosis and treatment of immune related disorders, e.g.  
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
PT thyroiditis and diabetes mellitus -  
XX  
XX  
PS Claim 48; Fig 3; 218bp; English.  
XX  
XX The present sequence is one of thirty three nucleic acids encoding PRO  
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
CC antagonists are useful for treating and diagnosing immune related  
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases.  
XX  
SQ Sequence 1114 BP; 188 A; 379 C; 356 G; 191 T; 0 other;

Query Match 94.6%; Score 1019; DB 22; Length 1114;  
Best Local Similarity 100.0%; Pred. No. 1.2e-179;  
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QY 181 cccccaagcacttctgctgctgctgctgctgctgctgctgctgctgctgctg 240  
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RESULT 14  
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XX  
XX 21-MAY-1999 (first entry)  
XX  
DE Human tumour necrosis factor receptor ZTNFR-5 cDNA.  
XX  
XX ZTNFR-5; tumour necrosis factor receptor; TNFR; human;  
XX cell maturation; bone cell regulation; ss.  
XX  
XX Homo sapiens.  
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XX Key location/Qualifiers  
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XX /note= "this region is specifically claimed in  
XX Claim 13(a)"  
XX  
XX MO9904001-A1.  
XX  
XX 28-JAN-1999.  
XX  
XX 21-JUL-1998; 98WO-US15072.  
XX  
XX 21-JUL-1997; 97US-0053203.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Farrah TM;  
XX  
XX MPI: 1999-132245/11.  
XX P-PSDB; AAW97749.  
XX  
XX Novel tumour necrosis factor receptor ZTNFR5 - useful for  
XX regulating maturation of TNF-ligand bearing cells  
XX  
XX Claim 13(e); Page 82-85; 109pp; English.  
XX  
XX This DNA sequence codes for a new, secreted tumour necrosis factor  
XX receptor (see AAW97749), designated ZTNFR-5. Novel ZTNFR-5 encoding  
XX polynucleotides and polypeptides were initially identified by  
XX querying an expressed sequence tag (EST) database for sequences  
XX homologous to conserved motifs within the TNF receptor family.  
XX Based on this search, a contig of 16 ESTs was constructed. ZTNFR-5  
XX polypeptides comprise 4 cysteine-rich repeats (see AAW97750-55) that  
XX are homologous to other TNF receptors. In particular the soluble,  
XX secreted TNF receptor osteoprotegerin. ZTNFR-5 polypeptide can be  
XX prepared by recombinant methods. The polypeptide, especially the  
XX extracellular domain, can be used to generate a soluble variant of  
XX ZTNFR-5. The polypeptides and nucleic acids can be used to screen  
XX for agonists and antagonists of ZTNFR-5. The polypeptides can be  
XX used in bone cell regulation and to regulate the maturation of TNF

CC ligand-bearing cells such as T- or B-cells, lymphocytes, peripheral  
CC blood mononuclear cells, polymorphonuclear leukocytes, fibroblasts  
CC or haematopoietic cells.  
XX  
XX Sequence 1205 BP; 205 A; 407 C; 386 G; 207 T; 0 other;

Query Match 94.6%; Score 1019; DB 20; Length 1205;  
Best Local Similarity 100.0%; Pred. No. 1.2e-179;  
Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctctccctgctccagcaagaccatgagcgctggagggccagcgtctgctgctg 60  
DB 159 gctctccctgctccagcaagaccatgagcgctggagggccagcgtctgctgctg 218  
QY 61 tgcctggtgttgccgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 120  
DB 219 tgcctggtgttgccgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 278  
QY 121 acacccacctacccttgcgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 180  
DB 279 acacccacctacccttgcgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 338  
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DB 399 tctccacccgcccac 458  
QY 301 gctcctctgcggagagcgctgag 360  
DB 459 gctcctctgcggagagcgctgag 518  
QY 361 tgcgcgtgc 420  
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QY 421 ccaacctggtgcggcgcgatctgc 480  
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DB 819 cgtgc 878  
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QY 841 ctgtgtggtgtgtgcagagcgctgcgctgcagagatgcgcggcgctgcagagatgc 900  
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OM of: US-09-006-352-1 to: PIR\_68: \* out-format : pfs

Date: Oct 31, 2001 12:32 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

#### Command line parameters:

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-O=/cgn2_1/USPTO_spool/US09006352/runat_30102001_104617_3292/app-query.fasta_1.1150  
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-MINMATCH=0.100 -IOOPCL=0.000 -IOOPEXT=0.000 -QGAPOP=4.500  
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELLOP=6.000  
-DELXT=7.000 -START=1 -MATRIX=bloms62 -TRANS=human40.cdi  
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-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0  
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#### Search information block:

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Query: US-09-006-352-1  
Query Length: 1077  
Database: PIR_68: *  
Database sequences: 219241  
Database length: 76174552  
Search time (sec): 48.020000
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#### score\_list:

Sequence	Strd Orig	ZScore	Escore	len	Documentation
PIR2:T45294	541.00	5.5e-25	1161	1	hypothetical protein KIAA1088
PIR1:A3536	355.00	381.11	6.6e-14	461	tumor necrosis factor receptor
PIR2:T48864	342.50	367.83	3.7e-13	459	tumor necrosis factor receptor
PIR2:B38654	340.00	364.94	5.1e-13	474	tumor necrosis factor receptor
PIR2:T54182	315.00	338.91	1.6e-11	435	tumor necrosis factor receptor
PIR2:T72175	262.50	284.51	2.1e-08	349	G2R protein - varicella minor vir
PIR2:T36858	262.50	284.51	2.1e-08	349	gene G4R protein - varicella viru
PIR2:T28623	262.00	284.00	2.3e-08	348	hypothetical protein G4R - vari
PIR2:T42086	241.00	257.93	3.7e-07	595	CD30 antigen precursor - human
PIR2:T43692	236.50	257.32	7.4e-07	325	T2 protein - rabbit fibroma vir
PIR2:T43783	230.50	251.50	1.8e-06	277	Ox40 antigen precursor - rat
PIR2:T37552	230.00	231.26	2.5e-05	277	Ox40 homolog - human
PIR2:T75518	224.00	237.46	3.7e-06	839	hypothetical protein - Deinoco
PIR2:T44768	216.50	232.95	1.1e-05	507	antifreeze glycopeptide AFGP pc
PIR1:GQV2ML	215.50	234.93	1.3e-05	326	T2 protein - myxoma virus (strd
PIR2:T60771	211.00	231.26	2.5e-05	277	B-cell activation protein CDA0
PIR2:T48700	210.00	230.32	2.8e-05	305	gene Ox40 protein - mouse
PIR2:T46476	203.00	222.08	7.2e-05	427	B cell-associated surface molec
PIR1:GQHNH	188.50	204.31	0.0005	427	nerve growth factor receptor pr
PIR1:T45219	187.50	195.27	0.0005	1356	N-methyl-D-aspartate receptor
PIR2:T44112	186.00	199.00	0.0007	627	spidrolin 2, dragline silk fibro
PIR2:B32393	185.00	204.11	0.0009	256	T-cell antigen 4-1BB precursor
PIR1:EDBE1F	181.50	188.37	0.0011	1460	Immediate-early protein IE180
PIR1:A26431	181.00	196.36	0.0014	425	nerve growth factor receptor pr
PIR1:EDBE11	180.50	191.68	0.0014	775	Immediate-early protein IE110 -
PIR2:T13954	180.50	186.79	0.0013	1574	MGEF6 protein - rat
PIR2:T44112	180.00	192.61	0.0015	627	spidrolin 2, dragline silk fibro
PIR1:Q00B3	179.50	191.72	0.0016	660	BHLFI protein - human herpesvir
PIR2:T42215	179.50	177.25	0.0013	7376	Immediate-early protein IE110 -
PIR1:EDBE11	179.00	190.08	0.0017	775	Immediate-early protein IE110 -
PIR2:T31338	178.00	180.56	0.0017	2639	fibroin - Chinese oak silkworm
PIR1:Q00B3	177.50	189.59	0.0022	660	BHLFI protein - human herpesvir
PIR2:T36729	176.50	189.46	0.0025	576	probable serine/threonine prote
PIR2:T31611	176.50	182.48	0.0022	1585	hypothetical protein Y5058A.9
PIR2:T51859	176.00	179.85	0.0021	1351	notch3 protein - human
PIR1:TN0006	176.00	191.18	0.0028	416	nerve growth factor receptor, 1
PIR2:T9265	175.00	181.95	0.0028	1357	hypothetical protein C0168.7 -
PIR2:T3846	174.00	192.42	0.0039	255	lymphocyte activation-induced
PIR2:T75477	173.00	185.06	0.0040	635	hypothetical protein - Deinoco
PIR2:T75420	172.50	185.28	0.0046	319	hypothetical protein - Deinoco

PIR2:T45294	-	172.50	187.42	0.0045	418	hypothetical protein T28P2.6
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seq\_name: PIR2:T45294

#### seq\_documentation\_block:

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hypothetical protein KIAA1088 [imported] - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 31-Jan-2000 #sequence-revision 31-Jan-2000 #text-change 21-Jul-2000  
C:Accession: T45294  
R:Kikuno, R.; Nagase, T.; Ishikawa, K.; Hirose, M.; Miyajima, N.; Tanaka, A.; Kotan  
DNA Res. 6, 197-205, 1999  
A:Title: Prediction of the coding sequences of unidentified human genes. XIV. The com  
A:Reference number: Z22961; MID:9937452  
A:Accession: T45294  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1161 <KIR>  
A:Cross-references: EMBL:AB029011; NID:95689512; PIDN:BA83040.1; PID:95689513  
C:Genetics:  
A:Note: KIAA1088
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#### alignment\_scores:

Quality	Ratio	Length	Gaps
541.00	5.35e	104	0
Percent Similarity: 97.115	Percent Identity: 97.115		

#### alignment\_block:

US-09-006-352-1 x T45294

Align seg 1/1 to: T45294 from: 1 to: 1161

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1074 aaIaValProGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyCys 1091  
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1108 GAlaAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaAla 1124  
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N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
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C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower,
```



Science 248, 1019-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
A:Reference number: A53356; MUID:90280639  
A:Accession: A53356  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMD>  
A:Cross-References: GB:M32315; NID:q189185; PIDN:AAA59929.1; PID:q189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.B.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,  
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <KOH>  
A:Cross-References: GB:M55994; GB:M3549; NID:q339757; PIDN:AAA36755.1; PID:q339758  
R:Demlic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.  
Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A:Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 23-461 <DEM>  
A:Cross-References: GB:563368; NID:q235648; PIDN:AA19824.1; PID:q235649  
A:Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)  
R:Keller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chan, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra  
A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
A:Cross-References: GB:M35857; NID:q339751; PIDN:AA63362.1; PID:q339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.  
J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec  
A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>  
R:Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A:Reference number: A35010; MUID:90110215  
A:Accession: A35010  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kühnert, P.; Kemper, O.; Wallach, D.  
Gene 150, 381-386, 1994  
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of  
A:Reference number: 138094; MUID:95121934  
A:Accession: 138094  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:Cross-References: EMBL:X80021; NID:q666044; PIDN:CAA56324.1; PID:q825701  
C:Genetics:  
A:Gene: GDB:TNFR2  
A:Cross-References: GDB:125914; OMIM:191191  
A:Map position: 1p36.2-1p36.2  
A:Introns: 26/3  
A:Note: The list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-22/Dominant: signal sequence #status predicted <SIG>  
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
F:40-76/Dominant: NGF receptor repeat homology <NGI>  
F:78-119/Dominant: NGF receptor repeat homology <NG2>

F:120-162/Dominant: NGF receptor repeat homology <NG3>  
F:164-201/Dominant: NGF receptor repeat homology <NG4>  
F:262-279/Dominant: transmembrane #status predicted <TMN>  
F:280-461/Dominant: intracellular #status predicted <INT>  
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

alignment\_scores:  
Quality: 355.00 Length: 334  
Ratio: 1.994 Gaps: 13  
Percent similarity: 53.293 Percent identity: 29.940

alignment\_block:  
US-09-006-352-1 x A53356

Align seg 1/1 to: A53356 from: 1 to: 461

```

10 GCTCCAGCAGGACATGAGGGCGCTGGAGGGCGGCGGCGCTGCTGCT 59
   |||||...:  |||||  :|||  |||||...|||
2  Alapvalalavaltrpalaaleu...Alavalglyeuleuleutr 17
   :|||:  |||||...|||
60 GTGCTGCTGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 109
   :|||:  |||||...|||
17 palalalalalalaleupola.....G 26
110 GAGTGGCAGAACACCCACCTGCGCGGAGCAGACAGGAGGAG 159
   |||||  |||||  |||  |||||
26 lvalalalalalalalapro.....gluproglyser 38
160 .....CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 173
39 Thrcysargleuarglutrtyrasplnthraladlmetcyscysse 55
   :|||:  |||||  |||||  |||||
174 CCAGTGGCCCCAGGACCTTTGTCAGGGCGCTGGCGGCGGAGACAGCC 223
   :|||:  |||||  :|||  |||  :|||
55 TLVcysSerProglglnhlsalalalvalphcysThrlySerla 72
224 CCAGCAGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 273
   |||||  |||  |||||  |||||  |||||  |||||
72 spltrValcysAspSerGcyluaBsertrhTytrhlglnleutrpan 88
274 TACCTGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323
   :|||:  |||||  |||||  |||||  |||||  |||||
89 TrpValProglucylsleuSerGylserarGcysSerSeraspInva 105
324 GGAGCAGCGGCTGTGCGCAGCCAGCAGCAGCTGCGCTGCGCGCGCA 373
   |||||  |||||  |||||  |||||  |||||  |||||
105 lglutrhGlnalacysThrarglucInasnarglIleCysThrCysargp 122
374 CCGGCTTCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 405
   |||||  |||||  |||||  |||||  |||||  |||||
122 roglytrptrycysalaleuSerlysglnlglucylsarglucysAla 138
406 GAGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 455
   :|||:  |||||  |||||  |||||  |||||  |||||
139 ProleuargylcysargProglpHeiglvalalalargProgluthgl 155
456 CAGCAGACAGCAGCTGCGCAGCGCTGCGCGCGCGCAGCAGCTTTCAG 505
   :|||:  |||||  |||||  |||||  |||||  |||||
155 urhSeraspvalalvalcylslysrProcysAlaProglThrphSerasp 172
506 GCAGCTCAGCTCAGAGAGTCCAGCCGCGCAGCCGCGCAGCTGCGCG 555
   :|||:  |||||  |||||  |||||  |||||  |||||
172 hrhTrSerSerThrAspIleCysArgProhlsGlnIleCysasnValal 188
556 GCGCTGGCCCTCAATGGCAGGCTTCTCCCATGACACCTGTGCGAC 605
   :|||:  |||||  |||||  |||||  |||||  |||||
189 Ala.....IleProglyasnAlasermetaspAlalalalysrh 201
606 CAGTGCAGTGGCTTCCCTCAGCAGCAGGCTGCGCAGGAGTGGAGAGT 655
   |||||  |||  :|||  :|||  :|||  :|||
201 rSerThrSer.....ProThrargSerMetAlaProglAlalalalal 216
```



```

656 GTGAGCGTCCGTCATCGACTTTGTGGCTTCCAGACATCCATCAG 705
    : : : : :
216 euProGlnProVal.....SerThrArgSerGln 225
    : : : : :
706 AGCGTCGACGCGCTGCTGACAGCCCTGACGCGCCGAG..... 744
    : : : : :
226 HisThrGlnProThrProGlnProSerThrAlaProSerThrSerPheLe 242
    : : : : :
745 ....GGCTGGGCTCCGACACCCAGGCGG.....GGCCGCGCGG 778
    : : : : :
242 uLeuProMetGlyProSerProProAlaGlnGlySerThrGlyAspPheA 259
    : : : : :
779 CCTGCGACGTGAAGCTGCGTGGCGGCTCAGCAGACCTCTGGGGCGCAG 828
    : : : : :
259 IaleuProValGlyLeuIleValGlyAlaThrAlaLeu..... 271
    : : : : :
829 GACGGGCGCTGCGTGGCGGCTGCTGAGCGGCTG.....CGCGT 869
    : : : : :
272 ...GlyLeuLeuIleIleGlyValValAsnGlyValIleMetThrGlnVa 287
    : : : : :
870 GCGCCAGCATGCC...GGGCTGAGACGAGCGCTCCGAGCGCTTCCTCC 916
    : : : : :
287 LlysLysLysProLeuGlyLeuGlnArgGlnAlaLysValProHisLeuP 304
    : : : : :
917 CT 918
    : : : : :
304 ro 304

```

seq\_name: p1r2:148854

```

seq_documentation_block:
gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
A:Accession: 148854
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A:Reference number: 148854; MUID:95178848
A:Accession: 148854
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-459 <RES>
A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F:151-188/Domain: NGF receptor repeat homology <NGF>

```

```

alignment_scores:
    quality: 342.50      length: 238
    ratio: 2.429        gaps: 10
Percent Similarity: 59.244      Percent Identity: 34.034

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alignment\_block:

US-09-006-352-1 x 148854 ..

Align seg 1/1 to: 148854 from: 1 to: 459

```

160 CGCGTGGTGGCGCCGACAGTCCCGCCAGGACCTTTGTGCGACGGCGCTG 209
    : : : : :
37 GlnMetCysAlaLysCysProProGlnGlnThrValLysHisLeuPheCys 53
    : : : : :
210 CCGCCGAGACAGCCCGACGAGCTGTGGCGGCTGTCACCGCGGCGACATPACA 259
    : : : : :
53 sAsnLysThrSerAspThrValCysAlaAspCysGlnAlaSerMetLysTyr 70
    : : : : :
260 CGCAGTTCTGAACTACTGGAGCGCTGCCGCTACTGACAGCGTCTCTGC 309
    : : : : :
70 hrGlnValTrpAsnGlnPheArgThrCysLeuSerCysSerSerSerCys 86
    : : : : :
310 GGGAGCGCTGAGGAGGAGCGGCTTGGCCAGCCGACCCAGCCAGCCGCGC 359
    : : : : :
87 SerThrAspGlnValGlnThrArgAlaCysThrLysGlnGlnAsnArgVa 103
    : : : : :

```

```

360 CTGCCCGTCCGCGACCGGCTTCTTC.....GGCAGCGCTGGTT 397
    : : : : :
103 LysAlaCysGlnAlaGlyArgTyrCysAlaLeuLysThrHisSerGlys 120
    : : : : :
398 TC.....TGCTGGAGACGCGATGCTGCACCTGCGTGGCGGCTG 438
    : : : : :
120 erCysArgGlnCysMetArgLeuSerLysCysGlyProGlyPheGlyVal 136
    : : : : :
439 APTGCCCGCGGACCCCGCCAGACAGACGAGTGGCCAGCGCTGCGCCCGC 488
    : : : : :
137 AlaSerSerArgAlaProAsnGlyAsnValLeuGlyLysAlaCysAlaLpr 153
    : : : : :
489 AGGACCTTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCAGGCCAGCC 538
    : : : : :
153 oGlyThrPheSerAspThrThrSerSerThrAspAlaCysArgProHisA 170
    : : : : :
539 GCAACTGACAGGCGCTGGGCTGGCCCTCAATGTGCGACAGGCTTCTCTCC 588
    : : : : :
170 rGlyCysSerIleLeuAla.....IleProGlyAsnAlaSer 182
    : : : : :
589 CATGACACCCGTCGACACAGCTGCAGCTGCTTCCCGCTCAGACAGCGT 638
    : : : : :
183 ThrAspAlaValCys.....Al 188
    : : : : :
639 ACCAGAGACTGAGAGTGTGAGCGTGCCTCATGCACTTGTGGCTTCC 688
    : : : : :
188 aPro.GluserProThrLeuSerAlaIleProArgThrLeuTyrValSer 204
    : : : : :
689 AGGACATCTCATCAGAGGCTGCAGCGGCTGTGTCAGCGCTCGAGGCC 738
    : : : : :
205 GlnProGlnProThrArg.SerGlnProLeuAspGlnLeuPro...GlyP 220
    : : : : :
739 CCGGA.....GGCGTGGGGTCC..... 755
    : : : : :
220 roSerGlnThrProSerThrLeuThrSerLeuGlySerThrProIleIle 236
    : : : : :
756 .....GACACCAAGGCGGG.....CCGGCGGCGCTTGCAGCTGA 790
    : : : : :
237 GluGlnSerThrLysGlyGlyIleSerLeuProIleGlyLeuIleValGln 253
    : : : : :
791 AGCTGCGCTCG 800
    : : : : :
253 yValThrSer 256
    : : : : :

```

seq\_name: p1r2:B38634

seq\_documentation\_block:

tumor necrosis factor receptor type 2 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999

C:Accession: B38634; A40254; S54816

R:Lewis, M.; Tarragila, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto

A:Reference number: A38634; MUID:91187885

A:Accession: B38634

A:Molecule type: mRNA

A:Residues: 1-474 <LEW>

A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828

R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J Mol. Cell. Biol. 11, 3020-3026, 1991

A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f

A:Reference number: A40254; MUID:91246168

A:Accession: A40254

A:Molecule type: mRNA

A:Residues: 1-474 <GOO>

A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828

R:Kisnerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995

A:Description: Characterization of the promoter region of the murine p75-TNF receptor

A:Reference number: S54816

A:Accession: S54816



A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-22 <KIS>  
A:Cross-references: EMBL:X87128; NID:g809043; PDB:1CA60618.1; PDB:g809044  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: cytokine receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F:40-77/Domain: NGF receptor repeat homology <NG1>  
F:79-120/Domain: NGF receptor repeat homology <NG2>  
F:166-203/Domain: NGF receptor repeat homology <NG4>

alignment\_scores:  
Quality: 340.00 Length: 278  
Ratio: 2.152 Gaps: 12  
Percent Similarity: 56.835 Percent Identity: 32.014

alignment\_block:  
US-09-006-352-1 x B38634 ..

Align seg 1/1 to: B38634 from: 1 to: 474

```
160 CGCGTGGTGGCGCCAGTGGCCCGACGACCTTGTGTGACGGCCGTG 209
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:
52 G1MeCysAlaLysCysProProG1nTyAlaLysHisPheCy 68
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
210 CCOCGAGACACCCCGGAGCGTGGCCGCTGTCCACCGCCGACTACA 259
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
68 sAnLysThrSerAspThrValCysAlaAspCysGluAlaSerMetTyrT 85
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
260 CGCAGTCTGAGACTACTGAGCGGCTGCGCTACTGCAACGCTCTCTGC 309
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
85 hrcInValIrrpAsnInIphEarThrcYsLeuSerSerSerSerCys 101
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
310 GGGGACGCTGAGGAGGACGCGGCTGGCCACGCCACACACGCTGC 359
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
102 ThrThrAspGlnValGluIleArgAlaLysThrLysGlnGlnAsnArg 118
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
360 CTGCGCCCTGCGCCAGCGGCTCTTC.....GGCGACGGCGT 397
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
118 LysAlaCysGlnAlaGlyArgTyrCysAlaLeuLysThrHisSerGly 135
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
398 TC.....TGCCTGAGCAGCAGCATCGTGTCCACCTGGTGGCGGTG 438
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
135 ercYsArgGlnCysMetArgLeuSerLysCysGlyProGlyPheGlyVal 151
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
439 ATTGCCCCGGGACCCCGACAGACAGCAGTGGCCAGCGTGCCTCC 488
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
152 AlAsSerArgAlaProAsnGlyAsnValLeuCysLysAlaLysLar 168
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
489 AGGCACTTCTGAGCCAGCAGCTCCAGCTCAGAGCAGTGCACGCCACC 538
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
168 ogLThrThrPheSerAspThrThrSerSerThrAspValCysArgProHis 185
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
539 GCAACTGCAGCGCCCTGGCGCTGGCCCTCAATGTGCAGAGCTTCTCTC 588
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
185 rglLecYsSerThrLeuAla.....IleProGlyAsnAlaSer 197
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
589 CATGACACCCCTGTGACACAGCTGCATGAGTCCCGCTCAGACACAGGT 638
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
198 ThrAspAlaValCys.....Al 203
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
639 ACCAGAGCTGAGAGTGTGAGCGTGCCTCATCGACTTTGTGGCTTTC 688
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
203 aPro.GluserProThrLeuSerAlaIleProArgThrLeuLysValSer 219
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
689 AGAGACTCTCCATCAAGAGGCTGCAGGGGCTGTGACAGCGCTCGAGGCC 738
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
220 GlnProGluProThrArg.SerGlnProLeuAspGlnGluPro..GlyP 235
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
739 CCGGA.....GGGCTGGGGTCC..... 755
```

```
235 roSerGlnThrProSerIleLeuThrSerLeuGlySerThrProIlelle 251
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
756 .....GACACAAAGGGCGG.....CCGGCGCGCTTCACACTCA 790
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
232 GluInSerThrLysGlyLysIleSerLeuProIleLeuIleValG1 268
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
791 AGCTGCGTGGCGGCTTCACAGACTTCCTGGGGGGCGACAGCGGCGCTG 840
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
268 yAlThrSerLeuGly.LeuLeuMetLeuGlyLeuValAsnCysIlelle 284
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
841 CTGTGTGCGCTGCTGCAGCGCGCTGCGCTGGCCAGATGCCCGGAGTGA 890
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
285 LeuValGln.....ArgLysLysLysProSerCysLeuG1 296
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
891 GCGAGGCGTCCGTGAGAGCGCTTCCTCCCT 918
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
296 nArgAspAlaLysValProHisValPro 305
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
```

seq\_name: p1r2:154182

seq\_documentation\_block:

tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000

C:Accession: I54182

R:Baens, M.; Chafanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.

Genomics 16, 214-218, 1993

A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq

A:Reference number: I54182; MUID:93252381

A:Accession: I54182

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-435 <RES>

A:Cross-references: GB:U04270; NID:g339761; PDB:AAA36757.1; PID:g339762

C:Gene: GDR:LTBR

A:Map position: 12p13.3-12p13.1

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

alignment\_scores:  
Quality: 315.00 Length: 280  
Ratio: 2.006 Gaps: 13  
Percent Similarity: 56.071 Percent Identity: 33.571

alignment\_block:  
US-09-006-352-1 x I54182 ..

Align seg 1/1 to: I54182 from: 1 to: 435

```
31 CCCTGAGAGGGGCGCAGCCCTGCTGCTGTGCTGTGTTGGCGCTGCC 80
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
6 AlAtThrSerAlaProGlyLeuAlaIrrpGlyProLeuValLeuGlyLeu 22
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
81 TGCCCTGTGCGGTCGCCGGCTGTACGGGAGTGGCAGAAACCCACACT 130
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
22 eGlyLeuLeuAlaAlaSerGlnProGlnAlaVal.....ProProT 36
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
131 AC.....CCCTGGCGGGAGCA.....GAG 150
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
36 yrlAserGlnAsnGlnThrCysAlrGAspGlnGlnLysGlyTrGlu 52
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
151 ACAGGGAGGAGGCTGTGTCGCCAGCGCCAGCGCCCGACAGCCTTGTGCA 200
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
53 ProGlnHisArgLecYsCysSerArgCysProProGlyThrTyrValSe 69
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
201 GCGGCGGTCGCCCGCGAGACGCCAGCAGCAGCTGTGGCCGCTGCACCGC 250
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
69 rAlaLysCysSerArgIleArgAspThrValCysAlaThrCysAlaGlu 86
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
251 GCCACTNACGACGATTCTGAACTACTG.....GAGCGCTGCCGC 291
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
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Mon Nov 5 08:22:34 2001

us-09-006-352-1.rpr

Page 6

A:Experimental source: strain India-1967, ssp. major, isolate ind3  
R:Kolyhalov, A.A.; Blinov, V.M.; Gytocov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Ero  
submitted to the EMBL Data Library, April 1992  
A:Description: Nucleotide sequence analysis of the region of Varicella virus xhoI F O H P  
A:Accession: S46868  
A:Reference number: S46868  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <NO>  
A:Cross-references: EMBL:M67117; NID:G516428; PID:CA947540.1; PID:G516449  
A:Experimental source: strain India-1967, isolate ind3  
R:Shchepkunov, S.N.; Blinov, V.M.; Sandakchiev, L.S.  
FEBS Lett. 319, 80-83, 1993  
A:Title: genes of varicella and vaccinia viruses necessary to overcome the host protective  
A:Reference number: S32385; MUID:93202281  
A:Accession: S32385  
A:Molecule type: DNA  
A:Residues: 31-168 <SHC>  
A:Cross-references: EMBL:X69198  
A:Experimental source: strain India-1967, ssp. major  
A:Genetics:  
C:Gene: GfR  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
F:32-66/Domain: NGF receptor repeat homology <NGF>  
F:66-109/Domain: NGF receptor repeat homology <NG2>  
F:110-151/Domain: NGF receptor repeat homology <NG3>

[illegible]

US-09-006-352-1 x D36858 .

Align seg 1/1 to: D36858 from: 1 to: 349

[illegible]

seq\_name: p1r2.T28623

seq\_documentation\_block: hypothetical protein G2R - variola major virus  
C:Species: Variola major virus  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T28623  
R:Kassinger, R.F.: Deposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au  
Nature 386, 748-751, 1993  
A:Title: Potential viral determinants in terminal regions of variola smallpox virus  
A:Reference number: 220488; MUID: q4088747  
A:Accession: T28623  
A:Status: preliminary; translated from GB/EMBL/DBDJB  
A:Molecule type: DNA  
A:Residues: 1-348 <MAS>  
A:Cross-references: EMBL:U22579; NID:9623595; PIDD:AAA60933.1; PID:q439102  
A:Experimental source: strain Bangladesh 1975  
A:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

alignment_scores:		
Quality:	262.00	Length: 208
Ratio:	2.259	Gaps: 4
Percent Similarity:	55.769	Percent Identity: 30.769

US-09-006-352-1 x T28623

```
,Align seg 1/1 to: T28623 from: 1 to: 348
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[illegible]











```

123 ValProCysProProGlyHisPhe.....SerProGlySerAsnGlnAl 137
525 GTGCCAGGCCCCCAGCCGCAATGTCAGAGCCCTTGCGCTGACCTCAATGTC 574
137 acYslySerProTrpThrAsnGlySerGlyLeuSerGlyLysGlnIleArgHisP 154
575 CAGGCTCTCTCCATGACACACCTGTGCACACCTGCATGCTGCTGCTCC 624
154 roLaserAsnSerLeuAspThrValCysGlnAspArgSer.....Leu 168
625 CTCAGCACACGATACCAAGC.....CTGAGGAGTGA 659
169 LeuAlaThrLeuLeu..TrpGluThrGlnArgThrThrPheArgProThrT 185
660 GCGTGGCTGATGACATTTGCTTCCAGACATCTCCATCAAGAGGC 709
185 hrValProSerThrThrValTrp...ProArgThrSer.GlnLeuProSe 200
710 TGCAGCGGCTGCTGACAGCCCTGAGGCCCGCA.....G 744
200 rThrProThrLeuValAlaProGlnGlyProAlaPheAlaValIleLeuG 217
745 GCGTGGGG 752
217 IyLeuGly 219
seq_name: p1r2:I37552

```

```

seq_documentation_block:
OX40 homolog - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C:Accession: I37552
R:Latza, U.; Durkop, H.; Schultze, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat
Eur. J. Immunol. 24, 677-683, 1994
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment
A:Reference number: I37552; MUID:94170844
A:Accession: I37552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C:Superfamily: CD27 antigen; NGF receptor repeat homology

```

```

alignment_scores:
Quality: 230.00 Length: 313
Ratio: 1.597 Gaps: 16
Percent Similarity: 46.006 Percent Identity: 27.796

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alignment_block:
US-09-006-352-1 x I37552 ..

```

```

Align seg 1/1 to: I37552 from: 1 to: 277

```

```

40 GGGCAGAGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 89
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
11 GlyProCysAlaAlaLeuLeuLeuLeuGlyLeuGlyLeuSerThrValTh 27
90 GCGGCTGCGGCTGTACGCGGAGTGGCAAAACCAACCACTACCCCTGGC 139
||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
27 rGlyLeuHisCysVal.....GlyAspThrTrpProSerA 39
140 GGGACGAGAGACAGAGGGAGCGGTGTGTGCGCCAGTGGCCGCCAGGC 189
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
39 snAspArg.....CysCysHisGluCysArgProGly 49
190 ACCTTTGTGACGCGCGTGGCCGAGACAGCCCAAGAGAGTGGGCC 239
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
50 AsnGlyMetValSerArgCysSerArgSerGlnAsnThrValCysArgPr 66
240 GTGTTCACCGCGGCACATACACGAGTTCTGGAACCTAC.....CTGAGC 283

```

```

66 ocYslyProGlyPheThrAsnAspValValSerSerLysProCysLysP 83
284 GTCGCGGCTACTGCACAGCTCTGCGGGAGCGGAGAGAGAGGACGG 333
83 rocYsThrTrpCysAsnLeuArgSerGly.....SerGlnArgLysGln 97
334 GCTTGCACGCGCCACACACACAGTGCCTGCGCTGCGCGCACCGGCTTCT 383
98 LeuYsThrAlaThrGlnAspThrValCysArgCysArgAlaGly..... 112
384 GCGGCACGCTGTTTCTGCTTGGACACACGATCTGTCACCTGGTGGCG 433
113 .....ThrGlnProLeuAspSerThrLysProGly.... 122
434 GCGTATTTGCCCCGGGACCCCGCCAGAACAGCAGATGCGACCGTGC 483
123 .....ValAspCysAlaProCys 128
484 CCCCCAGCAGCTTCTCAGCAGACGTCAGCTCAGCTCAGAGTGCACGC 533
129 ProProGlyHisPhe.....SerProGlyAspAsnGlnAlaCysArgPr 143
534 CCACCGCAGCTGCAAGGCCCTGGGCGCTGGCCCTCAGTGCAGGCTCTT 583
143 oTrpThrAsnCysThrLeuAlaGlyLysHisThrLeuGlnProAlaSerA 160
584 CTTCCCATGACACCCCTGTGCACAGC.....TGCACGTGGCTGCC 624
160 snSerSerAspAlaIleCysGlnAspArgAspProProAlaThrGlnPro 176
625 CTCAGCACAGGATACAGAGCTAGAGAGTGTGAGCTGCGCGCTCATGCA 674
177 GlnGluThrGlnGlyProProAla..ArgProIleThrValGlnProThrG 193
675 CTTTGTGGCTTCCAGACATCTCCATCAGAGGCTGCAGCGGCTGTGC 724
193 lValaTrp...ProArgThrSer..... 199
725 AGGCCCTGAGAGCCCGGAGGGCTGGGTCCGACACCAAGGGCGGCGGC 774
200 ..... 774
775 GCGGCTTGACAGTGAAGCTGCTGCGCGCTCAGCGAGCTGTGGGCGC 824
204 rArgPro.ValGlu.....ValProGly... 211
825 GCAGAGCGGCGGCTGCTGTGTCGCGCTGTCAGAGCGCTGCGGTGGCA 874
212 ...GlyArgAlaValAlaAlaIleLeuGlyLeuGlyLeuValLeuGly.. 226
875 GGATGCGCGGGCTGAGCGGAGCGCTGAGCGCTTCTGCTGCTGTGCAC 924
227 .....LeuLeuGlyProLeuAlaI 233
925 TGCATCGGCGCCCTCTATTATTCATCATCTT 959
233 leLeuLeuAla.....LeuThrLeuLeu 240
seq_name: p1r2:F75518

```

```

seq_documentation_block:
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75518
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.: Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: F75518

```



A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-839 <WHI>  
 A:Cross-references: GB:AE001904; GB:AE000513; NID:g6458129; PID:AAF10038.1; PID:g645814  
 A:Experimental source: strain R1  
 C:Genetics:  
 A:Gene: DR0458  
 A:Map position: 1  
 C:Superfamily: herpesvirus immediate-early protein IE10; RING finger homology

alignment\_scores:  
 Quality: 224.00 Length: 362  
 Ratio: 1.258 Gaps: 14  
 Percent Similarity: 49.171 Percent Identity: 30.110

alignment\_block:  
 US-09-006-352-1 x F75518 ..

Align seg 1/1 to: F75518 from: 1 to: 839

```

3 TCCTCCCTGCTCCAGCAGACGACCATGAGCGCTGGAGGGCCAGGCTCT 52
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
320 AlapromserserAlaAlaAlaProsnqluproAlaseroluprova 336
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
53 CGCTGCTGTGCTGTGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCT 86
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
336 lAlaGlyArgProGlyThrAlaAlaSerSerProGlySerAlaSerPro 353
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
87 .....GCTGCCGCTGCCGC 101
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
353 althValthrProargGlygluThrProasphrAlaAlaSerAlaGly 369
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
102 TGATCCGGATGGAGCAAAACCCACCTACCTCCCT..... 136
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
370 ThrProserAlaGlyArgValThr..ProAlaProAlaProserAlaSer 385
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
137 .....GGCGGACCCAGACAGAGGAGGCGGCTGGTGGCGCCAG 177
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
386 GluGlyAlaSerAlaAlaAlaArgThrProGlyAlaGlySerGluThrPro 402
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
178 TGCCCCCCAGCACCTTG.....TGACGGCGCC 206
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
402 olleProAlaThrProIleProAlaThrProAlaGlyArgSerSerGly 419
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
207 GTGCCCGCGAGACGCCACGAGCT.....GTGGCGCGGTGC 244
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
419 luserAlaGlyThrAlaAlaAlaArgProAsnAlaAlaProAlaProva 435
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
245 CACCGCGGACCACTACAGCAAGTTCTGGAACACTGAGCGCCCTGCCGAC 294
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
436 SerGluAspArgSerAspValSerGlyLeuProArgArgGluAspAlaPr 452
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
295 TGCAAGCTCTCTGGGGGAGCGCTGAGAGAGGACGGCTTCCACGC 344
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
452 oAlaGluSerSerProvaAlaAlaAlaSerProAlaArgGlyAlaSerSeA 469
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
345 CACCCCAACAGCTGCTGCCCTGCCCGCCACCGGCTTCTTGGGACAGCTG 394
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
469 lProSerSerAlaProAlaAlaAlaAlaPro.....SerArgAlaPro 483
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
395 GTTCTGCTTGGAGCAGCATGTCACCTGTGCGCGCGCTGATGCC 444
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
484 ValSerGlyGlySerValSer.....AlaProArgThrAlaPr 496
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
445 CCGCGGACCC.....CCAG 458
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
496 oThrAlaProvaAlaGluGluGlyAlaValProvalSerProserAlaA 513
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
459 CAGAAGACGAGTGGCAGCGCTGCCCGCCACGACCTTCTTACGACAGA 508
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
513 lAlaAlaProArgGlyGlyAlaSerSerAlaAlaAlaProserAlaProAla 529
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

```

```

509 GCTCCAGCTCAGACAGTGCACAGCCCAACCCCAACATGCAGCGCCCTGGCC 558
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
530 AlAlaAlaArgGlyGlySerGlyAlaAlaGlyAlaAlaGlyAlaAlaSer 546
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
559 CTGCCCTCAATGTGCCAGGCTCTCTCCATGCATACACACCTGGACCAAG 608
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
546 lAlaProAla.....AlaAlaArgProAlaGluThrProGlyAlaSerA 561
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
609 CTGACAGTGGCTTCCCTCCAGCAGCGAGGTACACAGAGCTGAGAGTGG 658
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
561 lAlaGlyAlaSerGlyGlyGlyGly.....Val 571
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
659 AGCGTGGCTCATCGACTTGTGCTTCCAGAGCATCTGCATCAGAGG 708
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
572 SerAlaArgProSerGlnGlyThrProSerGlyThrProAlaSerA 588
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
709 CTGCAGCGGCTGCTGCAGGCTCTCGAGGCCCGGAGGCTGGGCTCCGAC 758
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
588 lAlaProAlaAlaGlyArgProAlaGlyGlyGlySerGlySerGly 604
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
759 ACCAAGGCGGCGCGCGCTTGCACCTGACCTGAGCTGCGGAGCTCA 808
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
605 ThrSerGlySerGlySerGly...AlaProAlaAlaAlaArgProGly 620
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
809 CGGAGCTCTGCGGGGCGCA.....GGACGGG 834
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
620 nGlyGlySerGlyAspAlaProvalAspLeuGlyLeuThrSerGlyArg 637
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
835 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 884
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
637 lGlySerGlyAlaGlyAlaGlyAlaGlyAlaGlyThrGlyGlu..... 650
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
885 GCTGAGACGAGGCGCTCGAGCGCTCTCCCTCC 917
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
651 ThrGlyAlaGlyThrProserAlaSerArgPro 661
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

```

seq\_name: pIR2:T44768

seq\_documentation\_block:  
 antifreeze glycoprotein AFgp polypeptide precursor [Imported] - Boreogadus saida  
 C:Species: Boreogadus saida  
 C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
 R:Accession: T44768  
 R:Chem. L.: DeVries, A.L.; Cheng, C.H.C.  
 Proc. Natl. Acad. Sci. U.S.A. 94, 3817-3822, 1997  
 A:Title: Convergent evolution of antifreeze glycoproteins in Antarctic notothenioid f  
 A:Reference number: 222834; MUID:97268653  
 A:Accession: T44768  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-507 <CHP>  
 A:Cross-references: EMBL:U43200; NID:g2078482; PID:AA060129.1; PID:g2078483  
 C:Genetics:  
 A:Introns: 1/3

alignment\_scores:  
 Quality: 216.50 Length: 303  
 Ratio: 1.196 Gaps: 11  
 Percent Similarity: 59.736 Percent Identity: 29.703

alignment\_block:  
 US-09-006-352-1 x T44768 ..

Align seg 1/1 to: T44768 from: 1 to: 507

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1 GCTTCCTGCTCCAGCAGACCATGAGCGCTGGAGGGCCAGGCT 50
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
114 AlAlaThrAlaAlaThrAlaAlaThrAlaAlaThrAlaAlaThrProAla 130
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
51 GTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 100
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
130 gAlaAlaThrProAlaThrAlaAlaThrProAlaThrAlaAlaThrProA 147
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

```







Mon Nov 5 08:22:34 2001

179 ProValAsnAspThrSerCysThrThrThrAlaGly 190

us-09-006-352-1.rpt

Page 12



OM of: US-09-006-352-1 to: SwissProt\_39.\* out\_format : pfs

Date: Oct 31, 2001 12:38 PM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MODEL=itame+_12p.model -DEV=x1h  
-O=/cgn2_1/USPRO_spool/US09006352/runat_30102001_104618_3398/app-query.fasta_1.1150  
-DB=SwissProt_39 -OFMT=fastan -SUFFIX=rs -GAPO=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000  
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-YGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELDP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blissum62  
-THRX=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pcr  
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORM=ext -MINLEN=0 -MAXLEN=200000000  
-USER=US09006352 -EGCN1_1.43 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLFPY -WAIT -THREADS=1
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Search information block:

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Query: US-09-006-352-1  
Query length: 1077  
Database: SwissProt_39.*  
Database sequences: 93435  
Database length: 3425486  
Search time (sec): 27.95000
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score_list:
Sequence      Strd Orig      Zscore  EScore Len  Documentation
SwissProt_39:TNR2_HUMAN + 357.00 317.24 1.1e-10 461 | P20333 homo sapiens (human).
SwissProt_39:TNR2_MOUSE + 340.00 302.54 6.9e-10 474 | P25119 mus musculus (mouse).
SwissProt_39:TNRC_HUMAN + 315.00 281.70 1.1e-08 435 | P36941 homo sapiens (human).
SwissProt_39:TNRC_MOUSE + 290.00 260.63 1.7e-07 415 | P50284 mus musculus (mouse).
SwissProt_39:VC22_VARV + 262.50 238.20 3.6e-06 349 | P34015 variola virus. protei
SwissProt_39:CD30_HUMAN + 241.00 216.50 3.4e-05 595 | P28908 homo sapiens (huma
SwissProt_39:VT2_SEPKA + 236.50 216.41 6.3e-05 325 | P25943 shope fibroma virus (S
SwissProt_39:OX40_RAT + 230.50 212.42 0.0001 271 | P15753 rattus norvegicus (rat
SwissProt_39:OX40_HUMAN + 230.00 211.85 0.0001 277 | P43489 homo sapiens (human).
SwissProt_39:VT2_MXYVL + 215.50 189.44 0.0006 326 | P29625 myxoma virus (strain
SwissProt_39:T2D3_HUMAN + 211.50 189.27 0.0006 1083 | P000228 homo sapiens (human)
SwissProt_39:CD40_HUMAN + 211.00 195.61 0.0011 277 | P25942 mus musculus (human)
SwissProt_39:OX40_MOUSE + 210.00 194.87 0.0012 272 | P47741 mus musculus (mouse).
SwissProt_39:CD40_MOUSE + 203.00 188.51 0.0026 289 | P27512 mus musculus (mouse).
SwissProt_39:CD40_BOVIN + 202.00 188.10 0.0029 269 | P28203 bos taurus (bovine).
SwissProt_39:NGFR_HUMAN + 186.50 173.69 0.0116 427 | P348138 homo sapiens (human).
SwissProt_39:SPD2_NBPCL + 186.00 169.16 0.0141 627 | P46804 nephila claviipes (ort
SwissProt_39:ICP8_MOUSE + 185.00 173.88 0.0189 256 | P20334 mus musculus (mouse).
SwissProt_39:ICP8_RAT + 181.00 167.30 0.0264 425 | P07174 rattus norvegicus (rat
SwissProt_39:ICP8_HSV1 + 180.50 163.14 0.0247 775 | P08393 herpes simplex virus
SwissProt_39:SPD2_NBPCL + 180.00 164.03 0.0272 627 | P46804 nephila claviipes (ort
SwissProt_39:T2D3_HUMAN + 180.00 160.63 0.0244 1083 | P000228 homo sapiens (human)
SwissProt_39:YH1_EBV + 179.50 163.28 0.0285 660 | P03181 Epstein-Barr virus (str
SwissProt_39:ICP8_HSV1 + 179.00 161.86 0.0291 775 | P08393 herpes simplex virus
SwissProt_39:NGFR_HUMAN + 177.50 161.58 0.0354 660 | P03181 Epstein-Barr virus (str
SwissProt_39:NGFR_CHICK + 176.00 163.16 0.0458 416 | P18519 gallus gallus (chick
SwissProt_39:41B8_HUMAN + 174.00 164.50 0.0630 255 | P07011 homo sapiens (human).
SwissProt_39:TEBK_HUMAN + 171.50 164.81 0.0468 4289 | P22105 homo sapiens (human).
SwissProt_39:CA11_HUMAN + 171.00 151.26 0.0615 1464 | P02452 homo sapiens (human).
SwissProt_39:CA11_CHICK + 170.00 150.67 0.0687 1453 | P02457 gallus gallus (chick
SwissProt_39:YK82_MYCTU + 167.50 152.48 0.1042 721 | O10690 mycobacterium tuber
SwissProt_39:PASA_PIG + 167.00 156.87 0.1287 332 | O77772 sus scrofa (pig). fast
SwissProt_39:CA11_CANFA + 166.50 147.23 0.1008 1460 | O98517 canis familiaris (do
SwissProt_39:NTC3_MOUSE + 166.00 144.36 0.0918 2318 | P281982 mus musculus (mouse)
SwissProt_39:ICP8_HSV2H + 166.00 150.36 0.1195 825 | P281982 herpes simplex virus
SwissProt_39:NME4_MOUSE + 166.00 147.42 0.1086 1323 | O03391 mus musculus (mouse)
SwissProt_39:ICP4_HSV1 + 164.50 146.26 0.1285 1298 | P08392 herpes simplex virus
SwissProt_39:IE18_PPVKA + 164.50 145.58 0.1257 1446 | P33479 pseudorabies virus (
SwissProt_39:IE18_MOUSE + 164.50 139.85 0.1043 3635 | O61001 mus musculus (mouse)
SwissProt_39:CA44_HUMAN + 164.00 144.19 0.1287 1690 | P53420 homo sapiens (human)
```

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seq_name: SwissProt_39:TNR2_HUMAN
seq_documentation_block:
ID TNR2_HUMAN STANDARD: PRT: 461 AA.
AC P20333:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
DE BLINDING PROTEIN 2) (TPP1) (P80) (TNF-R2) (P75) (CD120b) (ETANRECEPT).
GN TNFRSF10 or TNFR2 or TNFR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90260639; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Power S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins."
RL Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hele K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor."
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299745; PubMed=8661109;
RA Bellinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepallier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene."
RL Genomics 35:94-100(1996).
RN [4]
RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=90349572; PubMed=2169946;
RA Heiler R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [5]
RP SEQUENCE OF 27-31.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors."
RL J. Biol. Chem. 265:1531-1536(1990).
RN [6]
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE=91056048; PubMed=2173696;
RA Loetscher H., Schlaeeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HU60 cells."
RL J. Biol. Chem. 265:20131-20138(1990).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=93016040; PubMed=1328224;
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
```



RA	Llpari M.T., Goeddel D.V. ;
RX	"Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT	Characterization of ligand binding, internalization, and receptor phosphorylation."
RL	J. Biol. Chem. 267:21172-21178(1992).
RM	[8]
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.
RX	MEDLINE=99221490; Pubmed=10206649;
RA	Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H. ;
RT	"Structural basis for self-association and receptor recognition of human TRAF2."
RL	Nature 398:533-538(1999).
CC	- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	- PTM: PHOSPHORYLATED; MAINTAIN ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.
CC	- PHARMACOLOGICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND WEIER-AVERTIS). USED TO TREAT MODERATE TO SEVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND BINDING PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
CC	- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC	- DATAASE: NAME=PROW; NOTE=CD guide CD120b entry.
CC	WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm"
CC	- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel; WWW="http://www.enbrelinfo.com/"
CC	-----
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CC	-----
DR	EMBL: M32315; AAA59929.1; -
DR	EMBL: M35857; AAA63262.1; -
DR	EMBL: U52165; AAC50622.1; -
DR	EMBL: U52156; AAC50622.1; JOINED
DR	EMBL: U52157; AAC50622.1; JOINED
DR	EMBL: U52158; AAC50622.1; JOINED
DR	EMBL: U52159; AAC50622.1; JOINED
DR	EMBL: U52160; AAC50622.1; JOINED
DR	EMBL: U52161; AAC50622.1; JOINED
DR	EMBL: U52162; AAC50622.1; JOINED
DR	EMBL: U52163; AAC50622.1; JOINED
DR	EMBL: U52164; AAC50622.1; JOINED
DR	EMBL: M55994; AAA36755.1; -
DR	PIR: A35356; A35356
DR	PIR: A36007; A36007
DR	PIR: A36475; A36475
DR	PIR: B35010; B35010
DR	PIR: A23666; A23666
DR	PDB: 1CA9; 12-APR-99.
DR	MMI: 191191; -
DR	InterPro: IPR001368; -
DR	Pfam: PF00020; TNFR_G6; 4.
DR	PROSITE: PS00652; TNFR_NGFR_1; 2.
DR	PROSITE: PS00050; TNFR_NGFR_2; 4.
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Phosphorylation; Pharmaceutical; 3D-structure.
FT	SIGNAL
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FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DOMAIN
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FT	REPEAT
FT	REPEAT
FT	REPEAT
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FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DOMAIN
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[illegible]



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189 Ala.....IleProGlyAsnAlaSerArgAspAlaValCysTh 201
606 CAGCTGCACGCTTCCCTCCACACGAGGTCACGAGCTGAGAGT 655
201 rSerThrSer.....ProThrArgSerMetAlaProGlyAlaValHisL 216
656 GTGAGCGTGGCGTCATGACACTTGTGGCTTCCAGACATCTCATCAG 705
216 euProGlnProVal.....SerThrArgSerGln 225
706 AGGCTGACGAGCGCTGCTGACAGCCCTGAGCCCGAGAG..... 744
226 HisThrGlnProThrProGlnProSerThrAlaProSerThrSerPheLe 242
745 ...GGCTGGGTCGACACCAAGGCG.....GGCGGCGCGG 778
242 uLeuProMetGlyProSerProAlaGlnGlySerThrGlyAspPheA 259
779 CCTTGACAGCTAAGCTGGTGGCGGCTGACGAGCTCTCTGGGGCGAG 828
259 IAlaProValGlyLeuIleValGlyValThrAlaLeu..... 271
829 GAGCGGCGCTGCTGTGCGGCTGCTGACGAGCGCTG.....CGCGT 869
272 ...GlyLeuLeuIleIleGlyValValAlaCysValIleMetThrGlnVa 287
870 GCGCCAGATGCCC...GGCTGAGACGAGCGCTGTCGACGCTTCCTCC 916
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917 CT 918
304 TO 304

seq_name: SwissProt_39:TNR2_MOUSE
seq_documentation_block:
ID TNR2_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;

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RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RC Tissue=Liver;
RA Kissenberghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL; M60469; AAA39752.1; -
DR EMBL; M59378; AAA40463.1; -
DR EMBL; U39488; AAA85021.1; -
DR EMBL; X87128; CAA60618.1; -
DR PIR; B38634; B38634.
DR HSSP; P19436; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 203 4 X TNFR-CYS.
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC...) (POTENTIAL).
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alignment\_scores: Quality: 340.00 Length: 278

Percent Similarity: 56.835 Percent Identity: 32.014

Alignment\_block: US-09-006-352-1 x TNR2\_MOUSE ..

Align seg 1/1 to: TNR2\_MOUSE from: 1 to: 474

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68 sasnlysrThrSerThrValCysAlaAspCysAlaAspCysAlaSerMetYrT 85

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260 CGCAGTTCTGGAACCTACCTGAGACCGCTCCGCTACGACAGCTCTCTGC 309
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102 ThrThrAspGlnValGlnIleargValacysThrlyscInlnasnarlyla 118
      ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
360 CTCGCCGTCGCCGACCGGCTCTCTC.....GCCGACGCTGGTT 397
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118 lcyalaacyglnualaglyargtyrcysalaleuylsThrHISerGlyS 135
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398 TC.....TCCTTGAGACACGACATGCTCCAGCTGGTGGCGGCGTG 438
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135 ercysarGlnCysMetIarGleuSerlyscysglyProGlyPheGlyVal 151
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439 ATGGCCCGGGGACACCCCGACGACACGACGACGACGACGACGACGACG 488
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152 AlseSerarGAlarProasndlyasvalleucylsIasIacysAlarP 168
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
489 AGGCACCTCTCAGCCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 538
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168 oglyThrPheSerAspThrThrSerThrAspValCysArgProHISa 185
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539 GCACACTGCACGGCCCTGGGCGCTGCCTCAATGTCGACGCTCTCTCTCC 588
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185 rgllecysserilleuAla.....lleProGlyAsnAlaSer 197
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589 CATGACACCGCTGTGCACAGCTGACGCTGCTCCCGCTCAGCACAGGCT 638
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198 ThrAspAlaValCys.....A 203
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639 ACCAGAGCTGAGAGAGTGTGACGCTGCCGCTATGACTTTGTGCTTTC 688
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203 apTo.gluSerProThrIleuSerAlaIleProArgThrIleuTyValSer 219
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689 AGGACATCTTCATCAAGAGGCTGACGCGCTGCTGACGCGCTGCGAGGCC 738
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220 GlnProGlnProThrArg.SerGlnProLeuAspGlnGluPro...GlyP 235
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
739 CCGGA.....GGGCTGGGGTCC..... 755
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235 roserGlnThrProserIleleuThrSerIleuGlySerThrProIlele 251
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756 .....GACACCAAGGGGG.....CCGCGGGCGCTTGACACTGA 790
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252 GlnGlnSerThrIleGlyGlyIleSerLeuProIleGlyLeuIleValaG 268
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
791 AGCTGGCTGGGGGCTGCACGAGCGCTGGGGCGCCGACGAGCGGGCGCTG 840
      ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
268 yAlThrSerIleuGly.LeuIleuIleuIleuValaIleuIleuIle 284
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841 CTGCTGGCGCTGCTGACGCGCTGCGCGTGGCCAGATGCGCGGCTGGA 890
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285 leuValGln.....ArgIlyIlyIlySerProserCysIleuG 296
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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93352381; PubMed=8486360;
RA Beens M., Chaffanet M., Cassiman J.J., den Hertog H., Marynen P.,
RT "construction and evaluation of a hncDNA library of human l2p
RL transcribed sequences derived from a somatic cell hybrid."
RN Genomics 16:214-218(1993).
RP [2]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfeld B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-Beta specific receptor."
RL Science 264:707-710(1994).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L04270; AAA36757.1;
DR HSSP: P25942; 1CDF.
DR MIM: 600979;
DR InterPro: IPR001368;
DR Pfam: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00500; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 32 227
FT TRAMEM 228 248
FT DOMAIN 249 435
FT DOMAIN 442 211
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FT REPEAT 125 168
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FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
SQ SHOUENDE 435 AA; 46709 MW; 624626b6022f56f CRC64;

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alignment_scores:
  Quality: 315.00      Length: 280
  Ratio: 2.006         Gaps: 13
  Percent Similarity: 56.071      Percent Identity: 33.571

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alignment\_block:

US-09-006-352-1 x TNRC\_HUMAN

Align seg 1/1 to: TNRC\_HUMAN from: 1 to: 435



[illegible]

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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LYBR OR TNFRC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; Pubmed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Mare C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; Pubmed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping."
RL Genomics 30:312-319(1995).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC -----
DR EMBL; U29173; AAA68864.1; -
DR EMBL; L38423; AAB00846.1; -
DR EMBL; U30798; AAB81334.1; -
DR HSSP; P25942; ICDF.
DR MGD; MGI:104875; Lbdr.
DR InterPro: IPR001368; -
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.
FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 213 4 X TNFR-CYS.
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 170 TNFR-CYS 3.
FT REPEAT 171 213 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 142 169 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 415 AA; 44956 MW; 259326A566AE661 CRC64;

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452 .CCCCAGCCAGAACGACGACTGCCAGCCGCGCCCGCCAGGACCTTCTC 500
RT      |||||      |||||      |||||      |||||
238 rProthAlaIaIaProAlaIaProAlaIaProAlaIaProAlaIaPro 255
501 AGCCAGCAGCTCCAGCTCAGACGAGTCCAGCCAGCCAGCACTGACGCG 550
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
255 rProAlaIaIaProAlaIaProAlaIaProAlaIaProAlaIaProAla 265
551 CCCCTGGGCGCTGGCCCTCAATGTGCCAGGCTCTTCCATGACACCCCTG 600
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
266 .....AlaIaIaProProProProProProPr 273
601 TGCACGACGCTGACACTGCTTCCCTCAGACGAGGTACGAGAGCTGA 650
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
273 oAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 285
651 GGAAGTGTAGAGGTGCGGTCATGACATTGTGGCTTTCAGACATCTTCCA 700
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
286 .....AlaGlyPro 288
701 TCAAGAGCGCTGACGCGCTGCTGACGCGCTCGAGCCCGGAGGCGTGC 750
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
289 .ProThrAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 299
751 GGTCCGACACCCAGGCGGCGCGCGCGCTGACGCTGAGTGCCTG 800
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
299 IaAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 315
801 GCGGCTGACGAGCTCGTGGGCGGCGGCGCGCTGCTGTGCTGGCG 850
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
316 AlAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 332
851 TGTCCAGCGCTGCGCTGCGCGAGATGCGCGCGCTGAGACGAGCGTGC 900
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
332 aAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 349
901 CGTGAGCGCTTCTCTCTGCTGCTGATCTGCGCCCTCT 941
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
349 aIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 362
seq_name: SwissProt_39:CD40_HUMAN
seq_documentation_block:
ID CD40_HUMAN STANDARD; PRT; 277 AA.
AC P25942;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40)
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
RN [2]
RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Rajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40";
RL Proteins 27:59-70(1997).
RN [3]
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=98266353; PubMed=9605317;
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,

```

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RA Zheng Z., Naismith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm"
CC
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DR EMBL: X60592; CAA43045.1; -
DR PIR: S04460; S04460.
DR PDB: 1CDE; 01-APR-97.
DR MM: 109535; -
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_c6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00505; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 277 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 x TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT DISULFID 26 37
FT DISULFID 38 51
FT DISULFID 41 59
FT DISULFID 62 77
FT DISULFID 83 103
FT DISULFID 105 119
FT DISULFID 111 116
FT DISULFID 125 143
FT CARBOHYD 133 153
FT CARBOHYD 180 180
FT SEQUENCE 277 AA; 30619 MW; BC8776EC2CA45680 CRC64;
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Quality: 211.00 Length: 151
Ratio: 2.512 Gaps: 3
Percent Similarity: 55.629 Percent Identity: 30.464
alignment_block:
US-09-006-352-1 x CD40_HUMAN ..
Align seq 1/1 to: CD40_HUMAN from: 1 to: 277
169 TGGCGCCAGTGGCCCCAGGACCTTGTGTGACGCGCGCTGCGCGAGGA 218
||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
38 CysSerLeuGlnProGlyGlnIleuValSerAspCysThrGluPh 54
219 CAGCCCAAGAGCTGTGCGCGTGTCCAGCGCCGACTACAGCAGTTCT 268
||| ||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| |||
54 eThrluThrGlnCysLeuProCysGlyGluSerGlnuPheLeuAspThr 71
269 GGAAGTGTAGAGGTGCGGTCATGACATTGTGGCTTTCAGACATCTT 309
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
71 rPaInArGgluThrHisCysHisGlnHisLysTyrcysAspProAsnLeu 87

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540 CAACTGACAGCGCCCTGGAGCCCTGCATGTCACAGGCTTCTCC 589
    |||||
143 rascuylthleuSerGlyuSgluSprgSerLeuValThrLeuP6lu 160
    |||||
590 ATGACACCCCTGCG.....ACAGCTGACAGCTTCCCTCCAGC 630
    |||||
160 euSpralValuGlyuSgluSprgSerLeuValThrLeuP6lu 176
    |||||
631 ACAGGCTACAGGCTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAG 680
    |||||
177 ThrGlnArgPro.ThrPheArgProThrThrValGlnSerThrValT 193
    |||||
681 GCGCTTCCAGACATCTGCATCAAGAGCTGACAGCTGCTGAGGCC 730
    |||||
193 rp...ProArgThrSer.GluLeuProSerProProThrLeuValThrPr 208
    |||||
731 TCGAGCCCGCGGA.....GGGCTGGGG 752
    |||||
208 ogLuglyProAlaPheAlaValLeuGluGlyLeuGly 220

seq_name: SwissProt_39:CD40_MOUSE

seq_documentation_block:
ID CD40_MOUSE STANDARD: PRT; 289 AA.
AC P27512;
DT 01-AUG-1992 (rel. 23, Created)
DT 01-OCT-1996 (rel. 34, last sequence update)
DT 15-JUL-1999 (rel. 38, last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
    species of murine CD40 upon B lymphocyte activation.";
RL J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN-BALB/C;
RA Torres R.M.;
RL Submitted (Sep-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
    Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";
RL J. Immunol. 149:3921-3926(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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    or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M83312; AAB08705.1; -
CC EMBL: M94126; AAA37404.1; -
CC EMBL: M94129; AAA37404.1; JOINED.
CC EMBL: M94128; AAA37404.1; JOINED.
CC EMBL: M94127; AAA37404.1; JOINED.
CC PIR: A46476; A46476.

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DR HSP: P25942; 1CDF.
DR MGD; MGI:88336; Tnfrsf5.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00505; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 20 289
FT DOMAIN 20 193
FT TRANSMEM 194 215
FT DOMAIN 216 289
FT DOMAIN 25 187
FT REPEAT 61 103
FT REPEAT 104 144
FT REPEAT 145 187
FT CARBOHYD 153 153
FT SEQUENCE 289 AA; 3211 MW; C791CB6D2FEA574E CRC64;

DR HSP: P25942; 1CDF.
DR MGD; MGI:88336; Tnfrsf5.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00505; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 20 289
FT DOMAIN 20 193
FT TRANSMEM 194 215
FT DOMAIN 216 289
FT DOMAIN 25 187
FT REPEAT 61 103
FT REPEAT 104 144
FT REPEAT 145 187
FT CARBOHYD 153 153
FT SEQUENCE 289 AA; 3211 MW; C791CB6D2FEA574E CRC64;

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## alignment\_scores:

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Quality: 203.00 Length: 151
Ratio: 2.538 Gaps: 3
Percent Similarity: 52.980 Percent Identity: 31.126

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## alignment\_block:

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US-09-006-352-1 x CD40_MOUSE

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Align seg 1/1 to: CD40_MOUSE from: 1 to: 289

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169 TGGCCCGACGTCGCCCCGACGACCTTTGTGACGCGCGCGCGGAGA 218
    ||| ||| |||||::: |||
38 CysAspLeuGlyGlnProGlySerArgLeuThrSerHisCysThrAlaLe 54
    ::| ||| ||| |||||
219 CAGCCCGACGACGCTGTGGCCGCTTCACCGCGCCGACGACGACGATTCT 268
    ::| ||| ||| |||||
54 uGluThrGlnCysHisProCysAspSerGlyGluPheSerAlaGlnT 71
    |||||
269 GGAAGTACTGAGACGCTGCG.....CGCTACTGCAAGCTCTCTGCG 309
    ||||| |||||
71 rPasnArgGlnIleArgCysHisGlnHisArgHisCysGluProAsnGln 87
    ||| ||| ::|
310 GGGAGCGCTGAGAGAGAGGACGCGCTGCGACGCGACCGACGACGCTGC 359
    ||| ||| ::|
88 GlyLeuArgValIlySylGluGlyThr.....AlaGluSerAspThrVa 102
    ::| ||| ::|
360 CTGCCGCTGCCGACCGCGCTTCTTCGCG.....CACGCTGATTCT 400
    ||| ||| ::|
102 IcyThrCysIlySylGluGlnHisCysThrSerIlyAspCysGluAlaC 119
    ::| ||| ::|
401 GCTTGGAGACGACGATCGTGTCCAGCTGTCGCGCGCGGTATGTCGCCGGGCG 450
    ||| ||| ::|
119 ySalGlnHisThrProCysIleProGlyPheGlyValMetGluMetAla 135
    ||| ||| ::|
451 ACCCGACCGACGACGACGACGACGCGCTGCGCGCGCGCGCGCGCGCGCTGC 500
    ||| ||| ::|
136 ThrGluThrThrAspThrValCysHisProCysProValGlyPhePheSe 152
    ||| ||| ::|
501 AGCCAGCGCTGCAGCTGCAGAGAGGACGCGCGCGCGCGCGCGCGCGCGG 550
    ||| ||| ::|
152 rAsnGlnSerSerLeuPheGluIlySylGlyProThrProThrSerCysGlu 169
    ||| ||| ::|
551 CCCGCGCGCTGCGCGCTGCATGTGCGACGCGCTTCTCTCCAGACGCGCTGC 600
    ||| ||| ::|
169 sPlyAsnLeuGluValLeuGlnIlySylGlyThrSerGlnThrAsnValIle 185
    ||| |||
601 TGC 603
    |||
186 Cys 186

seq_name: SwissProt_39:CD40_BOVIN

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seq_documentation_block:
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AC   Q28203;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
GN   TNFRSF5 OR CD40.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97281252; PubMed=9135560;
RA   Hirano A., Brown W.C., Estes D.M.;
RT   "Cloning, expression and biological function of the bovine CD40
RT   homologue: role in B-lymphocyte growth and differentiation in
RT   cattle.";
RL   Immunology 90:294-300(1997).
CC   -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC   -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -1- SIMILARITY: CONTAINS A TNF-RECEPTOR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb.slb.ch).
CC   -----
DR   EMBL: U57745; AAC48710.1; -.
DR   HSSP: P25942; ICDF.
DR   InterPro: IPR001368; -.
DR   Pfam: PF00020; TNFR_cf.4.
DR   PROSITE: PS00652; TNFR_NGFR_1; 1.
DR   PROSITE: PS50050; TNFR_NGFR_2; 1.
KW   Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL          1..19
FT   CHAIN           20..>269
FT   DOMAIN          20..193
FT   TRANSMEM       194..215
FT   DOMAIN          216..>269
FT   DOMAIN          25..187
FT   REPEAT          25..60
FT   REPEAT          61..103
FT   REPEAT          104..144
FT   REPEAT          145..187
FT   CARBOHYD        153..153
FT   CARBOHYD        180..180
FT   NON_TER         269
SQ   SEQUENCE        269 AA; 29983 MW; 7469033F30F95F387 CRC64;
alignment_scores:
Quality: 202.00      Length: 235
Ratio: 1.757         Gaps: 7
Percent Similarity: 48.936      Percent Identity: 28.511

alignment_block:
US-09-006-352-1 x CD40_BOVIN ..
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163 CTGGTGTGCGCCAGTGCCTTGTGTCAGCGGCGCGTGC 212
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36 LeuCyAspLeuCyAspLeuCyAspLeuValAspCys 52
    : : : ||| ||| ||| : : : : :
213 CGAGACAGACCCAGAGCGTGTGCGCGTGCACCGCCAGTACACGC 262
    : : : ||| ||| ||| : : : : :
52 rgIuValserLysThrGluCysGlnserCysGlyLysGlyLuphLeu 69

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```

263 AGTTCTGGAAC.....TACSTGAGAGCGTCCGCTACGACAGCTC 303
    : : ||||| ||| : : : : ||||| |||||
69 erThrTrpAsnArgGluLysTyrCysHisGlnHisArgTyrCysAsnPro 85
    : : : : : : : : : : : : : : : : : : : : : : : :
304 CTGCGCGGAGCGTGAAGAGCGGCA.....CGGG 335
    ||| ||| : : : : :
86 AsnLeuGlyLeuArgGlyGlnserGlnGlyThrLeuAsnThrAspThr 102
336 TTGGCAGCGACCCAGACAGCGTCCGCGCGCGCGGAGCGGCTGTGCG 385
    ||| : : : : : : : : : ||| : : : : :
102 eCyValCysValGlnGlyGlnHisCysThrSerHisThr..... 115
386 CGACAGCGGTCTTCTGCTGAGACAGCATGCTGATGCTGAGCGGCGG 435
    : : : : : ||| : : : : : ||| ||||| |||
116 .....CysGluSerCysThrProHisSerLeuCysLeuProGlyPheGly 130
436 GTGATTGCGCGCGGACCCAGACAGCGAGACAGAGTGCAGCGGCGCC 485
    ||| : : : : : ||| : : : : : ||| ||||| |||
131 ValLysGlnLeuAlaThrGlyLeuLeuAspThrValCysLupProCysP 147
486 CGCAGGACCTTCTGACAGCAGAGCTCCAGAGAGAGTGCAGAGCGCC 535
    ||| ||| ||||| ||||| : : : : : ||| : : : : :
147 oLeuGlyPhePheSerAsnValSerSerAlaPheGlnLysCysHisArgT 164
536 ACCGCAACTGCAGCGGCGCTGGGCTGAGCTCATGTGCCAGGCTCTCC 585
    : : : : : ||||| : : : : : ||| : : : : :
164 rPThrSerCysGluArgLysGlyLeuValGlnGlnHisValGlyThrAsn 180
586 TCCCATGACACCTGTGTGACAGCTGACAGCTGCTCCGCTCCAGACAG 635
    : : : : : ||||| |||||
181 LysThrAspValAlaCys.....GlyPheGlnSerArgMetLeu 193
636 CGTACACAGAGCTGAGAGCTGAGCGTGCAGCTGATGCTGAGTGTGCT 685
    ||| : : : : : ||||| : : : : : ||| :
193 gThrLeuValValIleProValThrMetGlyValLeuPheAlaValIleu 210
686 TCCAGGACATCTCATCAGAGAGCTGACAGCGGCTGCGAGCGGCTGAG 735
    : : : : : ||||| : : : : : ||| ||||| :
210 euValSerAlaCysIleArgAsnIleThrLysLysArgGln...LeuArg 225
736 GCCCGGAGGCGTGGGCTCGACACCAAGGCGGCGCGGCGGCTTGA 785
    ||| ||| : : : : : |||||
226 ProCysThrLeuTrp.....LeuLysGlyArgGlyLeuProTrpPar 238
786 GCTGACCTGCGTCCGCGGCTG.....ACGAGACTCTGCGGCGGCG 826
    : : : : : ||||| : : : : : |||||
238 gArgLeuIleArgArgIlePheProAlaProThrArgLeuSerGlyAla 255
827 AGGAC 831
    : : : : : |||
255 rGAsp 256

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OM of: US-09-006-352-1 to: SPTRMBL\_16.\* out\_format : pfs

Date: Oct 31, 2001 12:33 PM

About: Results were produced by the Gencore software, version 4.5,  
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#### Command line parameters:

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-O=/cgn2.1/USPTO_spool/US09006352/runat_30102001.104618.3376/app-query.fasta_1.1150
-DB=SPTRMBL_16 -OPMT=fastan -SUFFIX=rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOCL=0.000 -LOOEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAEXT=0.500
-EGAPOP=6.000 -DEGAEXT=7.000 -YGAPOP=10.000 -YGAEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blissum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pcr
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=2000000000
-USER=US09006352 -CGN1_1.147 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLAPY -WAIT -THREADS=1
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#### Search information block:

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Query length: 1077
Database: SPTRMBL_16.*
Database sequences: 425026
Database length: 13335027
Search time (sec): 68.61000
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SP_human:099784 + 541.00 626.64 9.6e-28 1161      099784 homo sapiens (human). h
SP_human:098771 + 533.00 616.25 3.0e-27 1400      098771 homo sapiens (human). d
SP_human:098402 + 533.00 630.26 7.0e-27 100      098402 homo sapiens (human). d
SP_human:000300 + 444.00 519.89 2.5e-21 401      000300 homo sapiens (human). os
SP_human:090407 + 440.50 516.25 4.2e-21 372      090407 homo sapiens (human). os
SP_human:008727 + 425.50 498.36 3.9e-20 401      008727 rattus norvegicus (rat). os
SP_human:008712 + 424.50 497.20 4.5e-20 401      008712 mus musculus (mouse). os
SP_vertebrate:09PUS0 + 395.00 464.50 4.0e-18 302      09PUS0 salvelinus fontinalis (t
SP_human:063327 + 342.50 401.01 9.0e-15 439      063327 mus musculus (mouse). tu
SP_human:016614 + 340.50 398.94 1.2e-14 459      016614 homo sapiens (human). tu
SP_human:088734 + 336.00 393.17 2.3e-14 482      088734 mus musculus (mouse). p8
SP_human:098734 + 292.00 340.21 1.5e-11 655      098734 mus musculus (mouse). d
SP_human:075509 + 289.00 336.71 2.4e-11 655      075509 homo sapiens (human). tu
SP_human:057277 + 282.50 332.79 7.5e-11 348      057277 monkeypox virus. tumor n
SP_human:057103 + 280.50 330.46 1.0e-10 348      057103 monkeypox virus. tumor n
SP_human:057108 + 276.00 325.21 1.0e-10 349      057108 monkeypox virus. tumor n
SP_human:057100 + 274.00 322.88 2.7e-10 349      057291 monkeypox virus. tumor n
SP_human:057291 + 274.00 322.88 2.7e-10 349      057101 monkeypox virus. tumor n
SP_human:057102 + 274.00 322.88 2.7e-10 349      057102 monkeypox virus. tumor n
SP_human:057099 + 263.00 321.72 3.1e-10 350      057099 monkeypox virus. tumor n
SP_human:057116 + 265.00 312.39 1.0e-09 355      057116 cowpox virus (cpv). tumor
SP_human:085308 + 264.50 311.73 1.1e-09 349      085308 cowpox virus (cpv). sec2
SP_human:057110 + 262.50 309.50 1.5e-09 349      057110 variola virus. tumor nec
SP_human:057111 + 262.50 309.50 1.5e-09 349      057111 variola virus. tumor nec
SP_human:089118 + 262.50 309.50 1.5e-09 349      089118 variola virus. somalia-1
SP_human:089098 + 262.50 308.94 1.6e-09 348      089098 variola virus. and vari2
SP_human:057112 + 262.00 308.94 1.6e-09 348      057112 variola virus. tumor nec
SP_human:085407 + 261.50 308.34 1.7e-09 349      085407 variola virus. homolog c
SP_human:057284 + 261.50 308.34 1.7e-09 349      057284 cowpox virus (cpv). strain c
SP_human:057098 + 258.50 306.01 2.3e-09 349      057098 cowpox virus (cpv). strain c
SP_human:057305 + 259.50 305.83 2.3e-09 360      057305 cowpox virus (cpv). tumor
SP_human:057118 + 258.50 304.81 2.7e-09 351      057118 cowpox virus (cpv). tumor
SP_human:057359 + 258.50 304.81 2.7e-09 351      057359 cowpox virus (cpv). h4f
SP_human:057120 + 257.50 303.68 3.1e-09 349      057120 cowpox virus (cpv). tumor
SP_human:057097 + 257.50 303.68 3.1e-09 349      057097 cowpox virus (cpv). tumor
SP_invertebrate:09GUCW7 + 256.50 294.08 2.5e-09 1514      09GUCW7 leishmania major. 184
SP_virus:057122 + 254.50 300.58 5.0e-09 326      057122 cowpox virus (cpv). tumor
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seq_name: sp_human:095407
seq_documentation_block:
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AC 095407:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1).
GN DCR3 OR TR6 OR TNFRSF6B.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Goddard P.J., Wood W.I., Guney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Bolstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer."
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.Y., Kwon B., Ni U., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis."
RL J. Biol. Chem. 274:13733-13736(1999).
```

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RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20122600; PubMed=10655513;
RA Pat C., Connolly B., Metzker M.B., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Gallaway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/DCR3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster."
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99000561; PubMed=99000561;
RA Matthews L.;
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RX MEDLINE=AF104419; AAD03056.1; -
RX EMBL: AF134240; AAD29688.1; -
RX EMBL: AF217796; AAF35244.1; -
RX EMBL: AF217793; AAF33685.1; -
RX EMBL: AF217794; AAF33686.1; -
RX EMBL: AF121845; CAC03668.1; -
RX HSSP: P25942; ICDF.
DR InterPro: IPR000361; -
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; -; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00502; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;
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Quality: 1634.00      Length: 300
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AC 09NZ71;		
DT 01-OCT-2000 (TREMblrel. 15, Created)		
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)		
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)		
DE HELICASE-LIKE PROTEIN NHL.		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
NCBI_TaxID=9606;		
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SEQUENCE FROM N.A.		
MEDLINE=20122600; PubMed=10655513;		
Bal C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V.,		
Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;		
"Overexpression of M68/DCR3 in human gastrointestinal tract tumors		
independent of gene amplification and its location in a four-gene		
cluster.";		
Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).		
EMBL AF217796; AAF35243.1;		
SEQUENCE 1400 AA; 152373 MW; F3F2BB93D48ED3D9 CRC64;		

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GN      BK3184A7.3
OS      Homo sapiens (Human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RL      Matthews L.;
RR      Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR      EMBL, AL121845; CAC16546.1; -.
FT      NON_TER
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US-09-006-352-1 x Q9H402 ..

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Align seq 1/1 to: Q9NZ71 from: 1 to: 1400

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1  Lysasprhnsicuglyalaglygalyalaargprovalmalalavalprogl 17
68  TGTTGGGGGCGTCCGCCGCTGCGCGGTGCGCGGTGTACCGGAGTGGCA 117
17  YValGlyAlaIaGlyProAlaIaGlyAlaGlyCysThrArgSerGlyIa 34
118  GAACACCCACCTTACCCCTGAGCGGAGACGACAGACAGAGGAGCGCGTGT 167
34  TgmsntfrrhnsleProleuAlaGlyTrrgrrgtsrprgGlyAlaAlaGly 50

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[illegible]

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seq_name: sp_human:000300
168 GTGGCCCCAGTGCCTCCACGACACTTTGTGGAAGCGCGCTGCCGCCAG 217
|||||
51 ValTrpProValProProlArgHisLeuCysAlaIalaIalValProProl 67
218 ACAAGCCCACAGACGTGTGGCCCTGTCCACCGCGCCTACACGCACTTC 267
|||||
67 ggInPrOHIsAsrValItPrProVaISerThrAlarProLeuHIsAlaVal 84
268 TGGAACTACTGGAGCGCTCCCGCTACTGCAGAAGCTCTTGCGGGGAGCG 317
|||||
84 eugIuleuProArgAlaleuProleuIeuGIIndrGrProleuArgrGLyAla 100

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1397 G1YAlA1a1aG1YAla1cYsProlvalP1roP1roA1roG1h1sLeuG1cysAla1a1a1 136  
206 CGGCCCCCGCAGACAGCCGCCAGACAGTGGGCCGTTCCACGCGGCAC 255  
1363 aValP1roP1roA1roG1n1roH1sAsPval1TrP1roval1sE1rTh1a1aP1ro1 138  
256 TAAACGAGATTTCGGAAC1AC1AC1CGAGAGCGGTGGCCGATACGCAACGTC1 305  
1380 euH1sAla1aVal1leuG1leuP1roG1YAla1eulP1roLeu1Gln1a1rP1ro 139  
306 CTGGCGGAGCCG 317  
1397 Leu1a1rG1YAla 1400

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AC	000300; 060236;		
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DT	01-JUL-1997 (TREMBLrel. 04, last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, last annotation update)		
DE	OSTEOCYTE-BERN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B). INTERF11B OR OPB OR OCIF.		
GN	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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seq_name: sp_human: Q9H402
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AAC      Q9H402:      PRELIMINARY;
DT      01-MAR-2001      (TREMBL) 15, Created)
DDT      01-MAR-2001      (TREMBL) 15, Last sequence update)
DE      01-MAR-2001      (TREMBL) 15, Last annotation update)
DEF      DJ583P15.9 (KIAA1088) (FRAGMENT).
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RC TISSUE=KIDNEY.  
RC MEDLINE=97262071. PubMed=9108485;  
RA Simonet W.S., Lacey D.L., Wondisan C.R., Kelley M., Chang M.-S.,  
RA Luehthy R., Nguyen H.O., Woodson S., Bennett L., Boone T., Shimanoto G.,  
RA Derose M., Elliott R., Colombiero A., Tan H.-L., Trail G., Sullivan J.,  
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
RA Suggs S., Boyle W.J.;



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Mon Nov 5 08:22:35 2001

us-09-006-352-1.rpt

Page 6

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Align seg 1/1 to: 008727 from: 1 to: 401

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26 ProlystylLeuHisIstyrAspProIunhrlYargIleuLeuGlyAsn 42
174 CCAAGTGGCCCCGAGGACCTTTCGACAGGGCCGTCGCGCCGAGACAGCC 223
175 CCAAGTGGCCCCGAGGACCTTTCGACAGGGCCGTCGCGCCGAGACAGCC 224
42 pLyCysAlaIarProGlyThTTrYleuYlGlnHisCysThrValAlaArgL 59
224 CCAAGAGCTGGGGCCGCTCCGACACCGCCGACCTCAAGCAGTTCTGGAC 273
273 CCAAGAGCTGGGGCCGCTCCGACACCGCCGACCTCAAGCAGTTCTGGAC 274
59 ysthrLeuGlyValIProGSpIarAspTrYserTrYlTrhAspSerTrhPis 75
274 TACCTGGAGGCGCTGCGGCTACTGACAGCTCCTCGCGGGAGAGCTGAGGA 323
323 TACCTGGAGGCGCTGCGGCTACTGACAGCTCCTCGCGGGAGAGCTGAGGA 324
76 ThrSerAspIuGlyValTrYcysSerProAlaYlGlnHisCysThrVal 92
324 GGAAGCCAGGCGCTTGGCCAGCCACCCACACCGCTGCGCTGCGCGCA 373
373 GGAAGCCAGGCGCTTGGCCAGCCACCCACACCGCTGCGCTGCGCGCA 374
92 rValYlGlnHisAspArgTrhHisAsnAlaGlyCysGluCysGluG 109
374 CCGGCTTCTTCCGGCAGCGCTGATTCTGCTTGGAGCAGCATGTGTCCA 423
423 CCGGCTTCTTCCGGCAGCGCTGATTCTGCTTGGAGCAGCATGTGTCCA 424
109 IuGlyAlaTrYleuGlnGluLeuGluIuphCysLeuYlHisArgSerCysPro 125
424 CCTGGTCCGCGGTGATTCGCCCGGCGCACCCCGCCAGACAGCAGTGTG 473
473 CCTGGTCCGCGGTGATTCGCCCGGCGCACCCCGCCAGACAGCAGTGTG 474
126 ProIlyLeuGlnYalLeuGlnAlaIalYlTrhProGluArgSnthrValCyl 142
474 CCAACGCTGGCCCCGAGCAGCCTTTCGACAGGAGAGTCCAGTGTGAGCC 523
523 CCAACGCTGGCCCCGAGCAGCCTTTCGACAGGAGAGTCCAGTGTGAGCC 524
142 slyArgCysProAspGlyPhePheSerGlyGlnTrhSerSerYlAlaP 159
524 AGTCCAGGCCCCGAGCAGCCTTTCGACAGGAGAGTCCAGTGTGAGCC 573
573 AGTCCAGGCCCCGAGCAGCCTTTCGACAGGAGAGTCCAGTGTGAGCC 574
159 roCysArgYlHisTrhAsnCysSerSerLeuGlnYleuLeuIleGln 175
574 CCAAGCTCTTCTCCCATCAGACCCGTGGACGACGCTGCGACGCTGCTGCC 623
623 CCAAGCTCTTCTCCCATCAGACCCGTGGACGACGCTGCGACGCTGCTGCC 624
176 LysIleGlnAlaTrhHisAspAsnVal.....CysSerClyAsnAr 189
624 CCGAGCAGCAGGAGTTCACGAGGAGTGGAGAG.....TGAGACCGTGGCG 667
667 CCGAGCAGCAGGAGTTCACGAGGAGTGGAGAG.....TGAGACCGTGGCG 668
189 glnAlaIarTrhGlnAsnCysGlyIleAspValTrhLeuGlyGlnGlnAlaP 206
668 TCATCAGCTTGTGGGCTTCAGACGACATTCATCAGAGGCTGCGAGCGG 717
717 TCATCAGCTTGTGGGCTTCAGACGACATTCATCAGAGGCTGCGAGCGG 718
206 hePheArgPheAlaValIProTrhTrYlIleIleProAsnTrpIleuSerVal 222
718 CTGCTGAGGCGCTC 732
223 LeuAlaAspSerLeu 227
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AC 008712: 070207;
DT 01-JUL-1997 (TReMBLeI, 04, Created)
DT 01-JUL-1997 (TReMBLeI, 04, Last sequence update)
DT 01-MAR-2001 (TReMBLeI, 16, Last annotation update)
DE OSTEOBLASTPREDERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR (OCIF)).

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OS TNFRSF1B OR OPG.  
OC MUSCULUS (Mouse).  
CC Pakayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
RA Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NB1\_TaxID=10090;  
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RN SEQUENCE FROM N.A.  
RP STRAIN-BALB/C; TISSUE=KIDNEY.  
RC MEDLINE=97262071; PubMed=9108485;  
RA Simenly W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
Liethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
Rader M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,  
Davy E., Bucay N., Resnau-dego L., Hughes T.M., Hall D., Pattison W.,  
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
Stiggs S., Boyle W.J.;  
RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
of bone density.";  
RL Cell 89:309-319(1997).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=129/Ola, AND NIH SWISS:  
RC MEDLINE=98382527; PubMed=9714833;  
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,  
Ra Higashio K.;  
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)  
gene and its expression in embryogenesis.";  
RL Gene 215:319-343(1998).  
CC - FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
STROMA CELLS AND OSTEOCLAST PROGENITORS.  
CC - SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).  
CC - TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND  
PLACENTA. NOT DETECTED IN SPLEEN.  
CC - DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
15 TO DAY 17.  
CC CC  
CC -1- SIMILARITY: CONTAINS A LA-NGF/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EXBL: U94331; AAB53708.1; -.  
DR EXBL: AB01398; BAA82869.1; -.  
DR EXBL: AB013903; BAA33388.1; -.  
DR EXBL: AB013899; BAA33388.1; JOINED.  
DR EXBL: AB013900; BAA33388.1; JOINED.  
DR EXBL: AB013901; BAA33388.1; JOINED.  
DR EXBL: AB013902; BAA33388.1; JOINED.  
DR HSSP: P25942; ICDF.  
DR MGJ: I09587; Trfcsflb.  
DR InterPro: IPRO00488; -.  
DR InterPro: IPRO01368; -.  
DR Pfam: PF00020; TNFR\_c6\_3.  
DR ProDom: PD000771; -.1.  
DR PROSITE: PS00017; DEATH\_DOMAIN: 1.  
DR PROSITE: PS00552; TNFR\_NCFR\_1; 1.  
DR PROSITE: PS00500; TNFR\_NCFR\_2; 2.  
DR SMART: SM00005; DEATH\_1.  
KW Glycoprotein; repeat; cytokine; signal.  
FT SIGNAL 1 21  
FT CHAIN 2 401  
FT DOMAIN 23 63  
FT REPEAT 23 63  
FT REPEAT 64 106  
FT REPEAT 107 143  
FT REPEAT 144 201  
FT DOMAIN 306 365  
FT DISULEID 44 54  
FT DISULEID 41 62  
FT DISULEID 65 80  
FT DISULEID 83 97  
FT DISULEID 87 105  
FT DISULEID 118 142

OSTEOPROTEGERIN.  
4 X TNFR-CYS.  
TNFR-CYS 1.  
TNFR-CYS 2.  
TNFR-CYS 3.  
TNFR-CYS 4.  
DEATH DOMAIN.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.  
BY SIMILARITY.







421 CCACCTGTGCGCGCGTATTCGCCCGGCGACCCCGACCCCGACGACGCGA 470  
 121 ProProGlyIYrGIYAlasnrThrGIYrProHISglAspThrGI 137  
 471 GTGCCAGCCGTCGCCCGCGACCTTCACGACGACGACGTCGACGCTG 520  
 137 uCysValGInCysGlnAlaGlyPheTyrSerGIuValSerSerAlaLysA 154  
 521 AGCGTGCAGCGCCCGACGACGTCGCGCGCTGGCGCTGCACCTTCAT 570  
 154 laThrCysLeuAlaGlnSerAsnCysLysValGlyLysLeuA9ValAl 170  
 571 GTGCCAGGCTCTTCCTCCATGACGACGTCGCGACGACGTCGACGCTG 620  
 171 LeuLysGlyGlnAspTrpHisAsnThrLeuLysAlaSerCys.....Ty 185  
 621 CCGGCTGACGACGCGGTCACGAGAGCTGAGAGTGTGACGCTGCGCTG 670  
 185 rAspLeuLysThrArg..AspGlyAlaGlnTrpLeuHISglL1leuLeu 201  
 671 TCACACTTTGTG.....GCTTTCAGGACATCTCCATCAAGAGCTGACG 714  
 201 rothrPhePheIleGlnLeuHISglThrMetGlyL1leLysArgMetArg 217  
 715 CGGCTGTCGAGCGCTCGAGCGCGCGGAGGCTGGGCTCGACACCGAAG 764  
 218 ArgLeu.....AlaMetArgLeuProGlnGlnLysLysLysProLe 232  
 765 GCGCGGCGCGCGCGCTTCACGACGTCGACGCTGCGCGGCTCGACGAGC 814  
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 247 hemetAsnSerTrpAsp 252

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 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MOD1  
 RX MEDLINE=95178848; PubMed=7873884;  
 RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;  
 RT Allelic variation of the type 2 tumor necrosis factor receptor  
 gene.";  
 RL Mamm. Genome 5:726-727(1994).  
 DR EMBL; X76401; CA53981.1; -.  
 DR HSSP; P19438; INCF.  
 DR InterPro; IPR001368; -.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00505; TNFR\_NGFR\_2; 3.  
 DR SMART; SM00208; TNFR; 1.  
 FT NON\_TER 1  
 FT VARIANT 87 1 S -> T.  
 FT VARIANT 93 93 T -> I.  
 FT VARIANT 268 268 F -> I.  
 FT VARIANT 345 345 S -> F.  
 FT VARIANT 421 421 Y -> C.  
 SO SEQUENCE 459 AA; 48686 MW; 6C51D2CFLC4626DF CRC64;

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 37 GlnMetCysAlaLysCysProGlnLysValLysHisPheCys 53  
 210 CCGCGGAGACAGCCCGACGACGTCGCGCGCTTCACCGCGCGACTTAA 259  
 53 sAsnLysThrSerAspThrValCysAlaAspCysGlnAlaSerMetLysT 70  
 260 CGCATTTCTGAACCTGAGAGCGCTGCGCGCTGCAAGCTCTCTGCG 309  
 70 hrGlnValITrpAsnGlnPheArgThrCysLeuSerCysSerSerSerCys 86  
 310 GGGAGGCGTGAGAGAGGAGGCGCGCTTCGACGCGCGCGCGCGCGG 359  
 87 serThrAspGlnValGlnThrArgAlaCysThrLysGlnGlnHisnArgVa 103  
 360 CTGCGCGCTGCCGCGCGCTCTTC.....CGCGACGCTGCTT 397  
 103 ICysAlaCysGlnAlaGlyArgTyrCysAlaLeuLysThrHisSerGlyS 120  
 398 TC.....TCCTGAGACGACATGATGTCGACGCTGCGCGCGG 438  
 120 erCysArgGlnCysMetArgLeuSerLysCysGlnProGlnPheGlyVal 136  
 439 ATTGCGCGCGGCGACCCCGACGACGACGACGCGCGCGCGCGCGCG 488  
 137 AlaserSerArgAlaProAsnGlnValLeuLysLysAlaCysAlaLys 153  
 489 AGGACCTTCCTCAGCGACGACGTCGACGTCGACGACGTCGACGCGCG 538  
 153 oGlyThrPheSerAspThrThrSerSerThrAspValCysArgProHisA 170  
 539 GCACCTGACGCGCGCTGCGCGCTGCGCGCTCATGTCGACGCTCTTCC 588  
 170 rGlyLeuSerLysLysLysLysLysLysLysLysLysLysLysLysLys 182  
 589 CATGACACCTGTGACGACGACGTCGACGCTGCTTCCCGCTCAGACGAG 638  
 183 ThrAspAlaValCys.....Al 188  
 639 ACCAGAGCTGAGAGTGTGACGTCGCGCGCTCATGACCTTTGCGCTTTC 688  
 188 apro.GluSerProThrLeuSerAlaIleProArgThrLeuLysValSer 204  
 689 AGGACATCTCCATCAAGAGCTGACGCGCTGTCGACGCGCTCGAGAG 738  
 205 GlnProLysProThrArg.SerGlnProLeuAspGlnapro.....GlyP 220  
 739 CCGGA.....GGGCTGGGGGCTCC..... 755  
 220 roserGlnThrProserIleLeuThrSerLeuGlySerThrProIleIle 236  
 756 .....GACACCAAGGCGCG.....CCGCGCGCGCTTCGACGCTA 790  
 237 GluGlnSerThrLysGlyLysLysLysLysLysLysLysLysLysLysLys 253  
 791 AGCTGCGTCG 800  
 253 yValThrSer 256  
 seq\_name: sp\_human:Q16042



seq\_documentation\_block:  
ID Q16042 PRELIMINARY; PRT; 439 AA.  
AC Q16042;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91370650; PubMed=1966549;  
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,  
RA Brochhaus M., Lesslauer W.;  
RT "Two human TNF receptors have similar extracellular, but distinct  
intracellular, domain sequences.";  
RL CytoKine 2:231-237(1990).  
DR EMBL; S63368; AAB19824.1; -.  
DR HSSP; P25942; ICDF.  
DR InterPro; IPR001368; -.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR PRODOM; PD000711; -; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00505; TNFR\_NGFR\_2; 3.  
DR SMART; SM00208; TNFR; 2.  
SQ SEQUENCE 439 AA; 46090 MW; FEBCE329CC67FE6 CRC64;

alignment\_scores:  
Quality: 340.50 Length: 300  
Ratio: 2.115 Gaps: 11  
Percent Similarity: 53.667 Percent Identity: 29.667

alignment\_block:  
US-09-006-352-1 x Q16042 ..

Align seg 1/1 to: Q16042 from: 1 to: 439

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112 GTGCAGAAACCCACCTACCCCTGCGGAGCCAGACAGGAG.. 159
||||| ||||| ||| |||||
5 ValAlaPheThrProTyrAlaPro.....GluProGlySerTh 17
160 .....CGCGTGTGTGCGCC 175
17 rCyArgLeuArgIuTyrIYrAspGlnThAlaGlnMetLysSerL 34
176 AGTGCACCCCGAGCAGCTTTGTGAGCGCGCGTCCGCGAGACGCCC 225
||||| ||||| ::::: ||| ::|
34 yScySerProGlyGlnHisAlaLysAlaPheCysThrLysThrSerLsp 50
226 AGCAGGTGTGCGCGCTGTCCACCGCCGACACTACACGCACTTGTGACTA 275
||||| ||| ||||| ||||| |||||
51 ThrValCysAspSerCysGluAspSerThrTyrThrGlnLeuTrpAspTr 67
276 CCTGAGAGCGTCCGCTACTGCAACAGTCTCTGCGGAGCGTGGAGAG 325
::: ||||| ||||| ||||| |||||
67 pValPProGlnCysLeuSerCysGlySerArgCysSerSerAspGlnValG 84
326 AGCAGCGGCTTGTCCAGCCAGCCAGCAACAGCTGCTGCGCGCGCAGC 375
||||| ||||| ::||| ||| |||||
84 lGutThrGlnAlaCysThrArgGlnGlnAsnArgIleCysThrCysArgPro 100
376 GCGTCTTTCGGCAGCGTGT.....TTCTGCTTGA 407
||||| ::|||
101 GlYrPtyrCysAlaLeuSerLysGlnGlnIuLysArgLeuCysAlaPr 117
408 GCAGCAGTCGTCACCTGTCGCGGCGGATGTCGCCGCGGAGCCAGCCCA 457
::||| ||||| ||||| |||||
117 oLeuArgLysCysArgProGlyPheGlyValAlaArgProGlyThrGln 134
458 GCCAGAACACGCGAGTCCAGCGCGTCCCGCCAGCAGCAGCTTCTCAGCAGC 507
```

```
seq_documentation_block:
ID Q88734 PRELIMINARY; PRT; 482 AA.
AC Q88734;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P80 TNF-ALPHA RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor Gene: Genomic Structure and
Characterization of the two Transcripts.";
RL Genomics 0:0-0(0).
DR EMBL; Y14619; CAA74969.1; -.
DR EMBL; Y14620; CAA74969.1; JOINED.
DR EMBL; Y14621; CAA74969.1; JOINED.
DR EMBL; Y14622; CAA74969.1; JOINED.
DR EMBL; Y14623; CAA74969.1; JOINED.
DR EMBL; Y14679; CAA74969.1; JOINED.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRODOM; PD000771; -; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00505; TNFR_NGFR_2; 3.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48F83C CRC64;

134 hrSerAspValValCysLysProCysAlaProGlyThrPheSerAsnThr 150
508 AGCTTCACAGAGACAGTGCAGCCCGCCAGCACTGACGAGCCCTGGG 557
: ||||| ||||| ||||| ||||| |||||
151 ThrSerThrAspIleCysArgProHisGlnIleCysAsnValValAl 167
558 CTTGCGCCCTCAATGTGCCAGGCTCTTCTCCACAGCAACCTGTGCACA 607
: ||||| ||||| ||||| ||||| |||||
167 a.....IleProGlyAsnAlaSerMetAspLysValLysThrS 180
608 CTTGCACTGCTTCCCTCCCTCAGACACAGGTAACAGAGCTGAGAGTGT 657
||| ||| ||| ||| ||| |||
180 erThrSer.....ProThrArgSerMetAlaProGlyAlaValHisLeu 194
658 GAGCGTCCGTCATCAGACTTGTGCTTCCAGACATCTCCATCAAGAG 707
::: |||
195 ProGlnProVal.....SerThrArgSerGlnI 204
708 GCTGAGCGCGCTGTGACAGCCCTGAGCCCGCGAG..... 744
: ||| ::| |||||
204 sThrGlnProThrProGlnProSerThrAlaProSerThrSerPheLeu 221
745 ..GGCTGGGTCCGACACCAAGGCG.....GGCCGCGGCGC 780
||||| ||||| |||
221 euProMetGlyProSerProProAlaGlnGlySerThrGlyAspPheAla 237
781 TTGCAGCTGAGAGCTGCGTGGCGGCTCAGAGCTCTCCGAGGAGGCGCAGCA 830
||| ||| |||
238 LeuProValGlyLeuIleValGlyValThrAlaLeu..... 249
831 CGGCGCGCTGCTGTGCGGCTGCTCAGAGCCCTG.....GGCGTGC 871
||| ||||| ::|||
250 .GlyLeuLeuIleGlyValAlaAsnGlyValIleMetThrGlnVal 266
872 CCAGAGTCC...GGCTGAGCGGAGCTGCTGAGCGCTTCTCTCCT 918
::: ||| ||||| |||||
266 yLysLysProLeuCysLeuGlnArgIleAlaLysValProHisLeuPro 282
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seq\_name: sp\_rodent:088734



alignment\_scores:                   Quality: 336.00                   Length: 245  
                                  Ratio: 2.366                   Gaps: 11  
Percent Similarity: 57.959           Percent Identity: 33.469

alignment\_block:  
US-09-006-352-1 x 088734 ..

Align seg 1/1 to: 088734 from: 1 to: 482

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160 CGGCTGCTGTCGCCAGTGCACCCGACGACCTTTGTCGAGCGGCTG 209
    ::::: |||||:::|||||:::|||||:::|||||::: ||
52 GImeCysCyAlAlaLysCysProProGlyGlnTyrAlaLysHisPheCy 68
210 CCGCCGA.....GACAGCCGACGAGCTGGGCC 238
    ||:::|||||:::|||||:::|||||:::|||||:::
68 sAsnLysThrSerAspThrValCysAlaAspSerAspThrValCysAla 85
239 CGTGTCCACCGCGCCCACTACACGAGCTTGGAGCTACCGAGCGCTGC 288
    ||| ||||| ||||| ||||| ||||| ||||| |||||
85 spCySGlnAlaSerMetLysThrGlnValItrPasnGlnPheAlaGlyTr 101
289 CGCTACTGCAAGCTCTCTGGGGGAGCGTGAAGAGGACGACGAGCTTG 338
    ||:::|||||:::|||||:::|||||:::|||||:::
102 LeuSerCysSerSerSerCysSerThrAspGlnValGlnThrArgAlaCy 118
339 CCAAGCCGACCCACACACCTGCTGCGCTGCGCGACCGGCTTCTTC... 384
    ||:::|||||:::|||||:::|||||:::|||||:::
118 sThrLysGlnGlnAsnArgValCysAlaCysGlnAlaGlyArgTyrCysA 135
385 .....CGGACGCTGGTTTC.....TGCTTGAGACGACGATCG 417
    ||:::|||||:::|||||:::|||||:::|||||:::
135 lAlaLysThrHisSerLysSerCysArgLncYsMetArgLeuSerLys 151
418 TGTCACTGTGTCGGGCGGATGTCGCCGAGACCCGACGACGACGAC 467
    ||| ||||| ||||| ||||| ||||| ||||| |||||
152 CyAGLProGlyPheGlyValAlaSerSerArgAlaProAsnGlyAsnVa 168
468 GCAATGCCAGCGCTGCTGCGGAGCGACCTTTCAGCCAGCAGCTCAGCT 517
    ::: ||::: ||| ||||| ||||| ||||| ||||| |||||
168 lLeuCyLysAlaCysAlaProGlyThrPheSerAspThrThrSerSerT 185
518 CAGAGCAGTGCAGCCGACCCGACGACGACGACGACGACGACGACG 567
    ::::: ||::: ||||| ||||| ||||| ||||| |||||
185 hAspValCysArgProHisArgLecYsSerLleLeuAla..... 198
568 AATGTGCAGGCTTCTGCTGACGACGACGACGACGACGACGACGAC 617
    ::: ||||| ||||| ||||| ||||| ||||| |||||
199 ...lIleProGlyAsnAlaSerThrAspAlaValCys..... 209
618 CTTCGCCCTCAGCAGGATACGAGGAGCTGAAGAGTGAAGAGCGGCC 667
210 .....AlaPro.GluSerProThrIleuSerAlaIle 219
668 TCATGCATTTGTGGCTTTCAGACATTCATCAAGAGGCTGACGGG 717
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
220 ProArgThrLeuArgValSerLncProGlyProThrArg.SerGlnProL 236
718 CTGCTCAGGCGCTGAGGCGCGGA.....GGG 746
    ||| ||||| ||||| ||||| ||||| ||||| |||||
236 euAspGlnIlePro...GlyProSerGlnThrProSerIleuThrSer 251
747 CTGGGGCTC.....GACACCAAGCGCGG..... 770
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
252 LeuGlySerThrProIleIleGlnGlnSerThrLysGlyGlyLleSerIle 268
771 .CGGCGCGCGCTTGCAGCTGAAGCTGCGTGC 800
    ||| ||||| ||||| ||||| ||||| ||||| |||||
268 uProIleGlyLeuIleValIleGlyValThrSer 278
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seq\_name: sp\_todent:09EPUS

seq\_documentation\_block:  
ID 09EPUS           PRELIMINARY;           PRT;           655 AA.  
AC 09EPUS;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DR6..  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Mus.  
OX NCBI\_TaxID-10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=KIDNEY;  
RA Isogeni D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,  
RA Minami M.,  
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6  
RT (DR6)".  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF322069; AAC38115.1.  
DR EMBL; AF322069; AAC38115.1.  
DR EMBL; AF322069; AAC38115.1.  
SQ SEQUENCE 655 AA: 71909 MW: 1497C1432799E4FB CRC64;

alignment\_scores:                   Quality: 292.00                   Length: 219  
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Percent Similarity: 54.338           Percent Identity: 33.333

alignment\_block:  
US-09-006-352-1 x 09EPUS ..

Align seg 1/1 to: 09EPUS from: 1 to: 655

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58 CTGTGCTGCTGTCGCCAGTGCACCCGACGACCTTTGTCGAGCGGCTG 107
    ::: ||||| ||||| ||||| ||||| ||||| |||||
30 LeuLeuLeuLeuLysPheLeuSerThrIleThrAlaGlnProGlnLys 46
108 CGGAGTGCAGAAACACCCAGCTACCCCTGCGGAGCGAGAGAGGG 157
    ::: ||||| ||||| ||||| ||||| ||||| |||||
46 sThrLeuSerLeuProGlyThrGlyArgHisValAlaArgThrThrCys 63
158 AGCGGCTGCTGTCGCCAGTGCACCCGACGACCTTTGTCGAGCGGCTG 207
    ::: ||||| ||||| ||||| ||||| ||||| |||||
63 lValLeuThrCysAspLysCysProAlaGlyThrGlyValSerGlnHis 79
208 TCCGCGGAGAGACGACCCGACGACGACGACGACGACGACGACGAC 257
    ::: ||||| ||||| ||||| ||||| ||||| |||||
80 CysThrAsnMetSerLeuArgValAlaCysSerSerCysProAlaGlyThr 96
258 CAGCGAGTTCGGAACCTACCTGAGCGGCTGCGGAGCTGACGAGCTCT 307
    ::: ||||| ||||| ||||| ||||| ||||| |||||
96 eThrArgHisGlnAsnGlyIleGlnArgCysHisAspCysGlnProC 113
308 GCGGAGAGCGTGAAGAGAGCGACGAGCTTGCACGCCACACACGCT 357
    ||| ||||| ||||| ||||| ||||| ||||| |||||
113 ySPProThrProMetIleGlnArgLeuProCysAlaAlaLeuThrAspArg 129
358 GCGTGCAGCTGTCGCCAGTGCACCCGACGACCTTTGTCGAGCGGCTG 407
    ||| ||||| ||||| ||||| ||||| ||||| |||||
130 GlnCysLleCysProProGlyMetLysIleSerAsnGlyThrCysAlaPr 146
408 GCAAGCATCGTGTCCAGCTGTCGCCAGTGCACCCGACGACCTTGCAG 457
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
146 oHisThrValCysProValGlyThrGlyValArgLysGlyThrGlnAla 163
458 GCGAGAAACAGCAGTGCAGCGGCTGCGGAGCTGACGAGCTTGTAGCAG 507
    ::::: ||||| ||||| ||||| ||||| ||||| |||||
163 sGlnLysValArgCysLysGlnCysAlaArgGlyThrPheSerAspVal 179
508 AGCTTCAGCTCAACAGAGTGCAGCGGACGACGACGACGACGACGACG 557
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
180 ProSerSerValMetLysCysAlaValAlaHisThrAspCysLeuGlnAs 196
```



```

558 CCGGCGCCATGTCAGGCGCTTCTCCCATGACACCGCTGTC.... 603
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
196 nleugluvallylsprogluthrlysgluthraspsalnvalcysglym 213
604 .....ACAGCTGACGTGCTCCCGCTCAGCA..... 631
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
213 etargleuphpheserSerthrasn..ProProserSerGlythrValTh 229
632 .....CCAGGTCACAGAGCTGAGAGTGTGAGCGCTGCCGTCAT 671
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
229 rpheserSerprogluthrMetglu.....SerHisaspValProserS 244
672 CGACT 676
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244 erthr 245
seq_name: sp_human:075509

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seq_documentation_block:
ID 075509 PRELIMINARY; PRT; 655 AA.
AC 075509;
DT 01-NOV-1998 (TEMBLrel.. 08, Created)
DT 01-NOV-1998 (TEMBLrel.. 16, Last sequence update)
DT 01-MAR-2001 (TEMBLrel.. 16, Last annotation update)
DE TNER-RELATED DEATH RECEPTOR-6 (DJ181J13.1) (DR6 (TNER-RELATED DEATH
DE RECEPTOR-6)).
DR6 OR DJ181J13.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G.,
RA Vincenz C., Aggarwal B.B., Dixit V.M.;
RT Identification and functional characterization of DR6, a novel death
RT domain-containing TNF receptor."
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Parker A.;
RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF068868; AAC34583.1; -.
DR EMBL; AL096801; CAB75692.1; -.
DR HSSP; P07174; INGR.
DR InterPro; IPR000488; -.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNER_c6; 4.
DR Pfam; PF00531; death; 1.
DR ProDom; PD000771; -. 1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNER_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNER_NGFR_2; 1.
DR SMART; SM00005; DEATH; 1.
KW Receptor.
SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

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alignment_scores:
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  Ratio: 2.676 Gaps: 3
  Percent Similarity: 55.670 Percent Identity: 34.536

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alignment_block:
US-09-006-352-1 x 075509 ..

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Align seg 1/1 to: 075509 from: 1 to: 655

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127 ACCTACCCCTGGCGGAGAGAGAGAGGCGGTGTGTGGCCCA 176
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53 ThrytargHisValaspArgAlaThrGlyGlnValLeuThrCysAspPly 69

```

```

177 GTGCCCCCAGGACCTTTGTGACAGGCGCGTGCAGGACAGCCCA 226
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
69 scySProAlaGlyThrTyValSerGlnHisCysThrAsnThrLeuA 86
227 CGAGCTGTGGCGCCGTCGACCGCCGCTACAGCAGCTTGTGACATAC 276
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
86 rValCysSerSerCysProValGlyThrPheThrArgHisGlnAsnGly 102
277 CTGAGCAGGCTCCCTACTGCAACGTCCTCGCGGGAGCGTAGAGAGA 326
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
103 lIleGlyuScyHisAspCysSerGlnProCysProTyrPromElIleG 119
327 GGCACGGGCTTGCCAGCGCCACCCACACACGTCGCTGCGCGCCGAC 376
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
119 uLysLeuProCysAlaAlaLeuThrAspArgGlyuScyThrCysPro 136
377 GCTTCTGCGCGCAGCGCTTCTGTCGAGACAGCATCGTTCGACCT 426
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
136 lYMetPheGlnSerAsnAlaThrCysAlaProHisThrValCysPro 152
427 GGTGCGCGCGTGTATGCGCGGCGACCCCGACCCAGACAGCAGCAG 476
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
153 GlyTrpGlyValArgLysLysGlyThrGlyThrGlnAspValArgCys 169
477 GCGGTGCGCGCGCGCGCGCGCTTCTGAGCAGCAGCTCAGCTCAG 526
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
169 sGlnCysAlaArgGlyThrPheSerAspValProSerSerValMetLys 186
527 GCGACCGCCCGCGACATGCGACGCGCTGCGCGCTGCGCTCATGTG 576
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
186 yLysAlaTyThrAspCysLeuSerGlnAsnLeuValAlaLysPro 202
577 GCGTCTCTCCCATGACACCGCTGTCAGCAGCTGCGCTGCGCTGCT 626
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
203 GlyThrLysGlyThrAspAsnValCysGlyThrLeuProSerPheSer 219
627 CAGCACCGAG...GTACGAGGAGCT..... 648
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
219 rSerThrSerProSerProGlyThrAlaIlePheProArgProGlnHis 236
649 ..GAGAGCTGTGAGCGCTGCGCTGATCGACT 676
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
236 etGluThrHisGlu.ValProSerSerThr 245

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seq_name: sp_virus:057277

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seq_documentation_block:
ID 057277 PRELIMINARY; PRT; 348 AA.
AC 057277;
DT 01-JUN-1998 (TEMBLrel.. 06, Created)
DT 01-JUN-1998 (TEMBLrel.. 06, Last sequence update)
DT 01-MAR-2001 (TEMBLrel.. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ZAIRE-1996(96-17), ZAIRE-1996 (96-16);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; U88543; AAB94378.1; -.
DR EMBL; U87841; AAB94358.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; -.
DR Pfam; PF00020; TNER_c6; 2.
DR ProDom; PD000771; -. 1.
DR PROSITE; PS00652; TNER_NGFR_1; 2.
DR PROSITE; PS00050; TNER_NGFR_2; 2.
DR SMART; SM00208; TNER; 1.
SQ SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2001, 09:41:15 ; Search time 1618.98 Seconds  
(without alignments)  
6288.356 Million cell updates/sec

Title: US-09-006-352-1

Perfect score: 1077

Sequence: 1 gctctccctgctccgcgaag.....aaaaaaaaaaaaaaaaaaaaa 1077

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
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6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
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13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
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25: gb\_est33:\*  
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32: gb\_est40:\*  
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116: gb\_est47:\*



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254: gb\_est185:\*  
255: gb\_est186:\*  
256: gb\_est187:\*  
257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.







```
RESULT 2
LOCUS BF339551
DEFINITION 874 bp mRNA EST 22-NOV-2000
602039016P1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186995
ACCESSION BF339551
VERSION BF339551.1 GI:11286006
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM9508 row: P column: 04
High quality sequence stop: 701.
Location/Qualifiers
1. 874
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4186995"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1; NotI;
Site:2; SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 129 a 299 c 301 g 145 t
ORIGIN
Query Match 56.7%; Score 610.8; DB 147; Length 874;
Best Local Similarity 89.6%; Pred. No. 7.6e-117;
Matches 679; Conservative 0; Mismatches 77; Indels 2; Gaps 2;
```

```
361 tgcgcgtgcgcagccagcgtcttcgcgcagcactgatttgcgttgagagacagcattgct 420
434 TGCCCGCTGCCCGACCGCGCTTCTTCGCGACGCTGGTTCTCTGGAGACGATCGTGT 493
421 ccactctgtgtgcgcgcgtgtattgcccgcgggagacccccagcagagaaacgcagtgcacgc 480
494 CCACTGTGTGCGGCGGCTATGTCGCCGACCCCGACCGACAGACACGAGTGCAGGCT 553
481 tgcgccccagcactcttcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
554 GCCCGCCAGCAACCTTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 612
541 aactgcagggcccttgagccttgccctcaatcgtgcagagctctctccatgcacccctg 600
613 AACTGCACGCGCTGGCGGCGCTGCGCTCAATGTCAGAGCTTCCTCCATGACACCTCG 672
601 tgcacagctgcactgtcttcctccctcagcagcagcagcagcagcagcagcagcagcagc 660
673 TGCGACCACTGCACTGCTGCTCCCTCAGCA -CAGGGTACAGAGTGTATGATGATGAG 731
661 cgtgcgcatacgaacttgctgtgtcttcacagacatctccatcaagagcgtcagcagcgtg 720
732 CGTGCCTGCTTCTGTGAGTTGTGGCTTCACAGCACTCTCCATCAAGAGGTGCGGTGG 791
721 ctgcagggccctgcagggcccgagggcgtggggtgcagc 758
792 GCCTTAGCCCGGAGGTGGGTCCCGCAGGCGGCGGC 829

RESULT 3
LOCUS BE878908
DEFINITION 617 bp mRNA EST 20-OCT-2000
601492609P1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894794 5',
ACCESSION BE878908
VERSION BE878908.1 GI:10327684
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 617)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: DCTD/DIR/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM9685 row: a column: 03
High quality sequence stop: 617.
Location/Qualifiers
1. 617
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3894794"
/clone_lib="NIH_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site:1; NotI;
Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 91 a 224 c 203 g 99 t
ORIGIN
Query Match 55.2%; Score 594; DB 141; Length 617;
```







ACCESSION AM083241 GI:6038393  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 692)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-buck, M.D., Ph.D. cDNA Library Preparation: Life  
 Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The  
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
 Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)  
 Seq primer: -400p from Gidco  
 High quality sequence stop: 414.  
 Location/Qualifiers  
 1..692

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2583534"
/clone_lib="NCI CGAP Co21"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: Cloned: Vector: PCWV-SPORF6; Site: 1; Salt; Site: 2; Nct1; Cloned unidirectionally. Primer: oligo dT. Normalized to Cot >500. Average insert size 1.04kb. Normalized version of NCI-CGAP-Co18. Library constructed by Life Technologies."

```

Query Match	52.6%;	Score 566.6;	DB 111;	Length 692;
Best Local Similarity	97.9%;	Pred. No. 1.1e-107;		
Matches 605; Conservative	0;	Mismatches 10;	Indels 3;	Gaps 3;

QY	404	tgagacgcatctgttccacctgtgtgcgagcgtgattgccccggagcccccaagcaga	463
Db	619	TGAGACGCGATGATGTTCACCT -GTGCGGCGTGATGTGCCGGGACGCCAGTGCACA	561
QY	464	acacgacagtgccagccgtgtcccccagacacttctcaagccagagctccagctcagagc	523
Db	560	ACACGCGATGCCAGCCGTCGCCCCNAGGACACTTCTAGCCACCAAGCTCCAGCTCAGAGC	501
QY	524	agtgccagccccacgcaactgcagcgccctggagccttcgaatgtgcagagctct	583
Db	500	AGTGCCAGCCCCACGCCAACCTGCAGGGCCCTGGGGCTTAAGTCCAGGCTCTT	441
QY	584	ctctccatgacacctgtgcacagctgcattgtctctccctctagacacaggtaccag	643
Db	440	CTTCCCATGACACCTCTGTGCACCACTCACTGTGCTTCCCTCAGACACAGGTTACAG	381
QY	644	gagctgaggaagtgtagcagtgccgttcacatctgacttgtgtgcttccaggaatccatca	703
Db	380	GACCTGAGGAGGTGTGAGCTGTGCCCATCACTTGTGCGCTTTCACGGAATCTGCATTA	321
QY	704	agagagctgcagcagcagctgcagcagggcccttcagagccccggagggctgaggttcgcagaccga	763
Db	320	AGAGGCTGCACGCCCTGTCTGACAGGCCCTGAGGGCCCCGGAGGGCTGGGGTCCACACCA	261
QY	764	ggagcgggccgcgcgagctctgcagctgaagc -tgctgtgcgagctcagcagagctccctgggg	822
Db	260	GGGCGGAGCCGGCGGCTTGTGACGTGAAATCTGGCTGGGGCTCAAGGGAGCTCTGGGG	201

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; catarrhini; Homiidae; Homo.			
	NCI-CCGAP	<a href="http://www.ncbi.nlm.nih.gov/ccgap">http://www.ncbi.nlm.nih.gov/ccgap</a> .		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: ccgap@remail.nih.gov			
	Life technologies catalog #: 11548-013			
	DNA sequencing by: Washington University Genome Sequencing Center			
	Clone distribution: NCI-CCGAP clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	<a href="http://www.bio.llnl.gov/dbp/imag/imag.html">www.bio.llnl.gov/dbp/imag/imag.html</a>			
	Seq primer: -400p from Gdbco			
	High quality sequence stop: 387.			

```

FEATURES
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' Location/Qualifiers
1..540
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="283232"
/clone_ib="NCI CGAP-Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site:1: Salt; Site:2: Nci1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
BASE COUNT
120 a 165 c 160 g 88 t 7 others
ORIGIN
.
```

[illegible]



Db	420	ACCAAGTGCACACTGGGCTTCGCCCTCAGCACCAAGGTACCAGAGAGCTGAGAGTGATGACGT	361
OY	664	ggcgtcatcgacttctgtgctttccaggaacatctcaatcaagaaggctgcagcgctctgt	723
Db	360	GCCGTCATCGACTTTGTGGCTTTCCAGGACAATCTCCATCAAGAAGAGCTCAGGGCTGCTG	301
OY	724	cagggcccctcaggaagccccgaaggagcgctgggggttcgcgaaccacaagaaggcgggccgcggcccttg	783
Db	300	CAGGCCCCTCGAGAGCCCCCGGAGAGGCTGGGGGTCCGACACCAAGGCGGGCCGCGGCCCTTGG	241
OY	784	cagctgaagactgtcgltcgagcgagctcaagagagctcctctggggggcgcaagaaagcgagcgctgtg	843
Db	240	CAGCTGAAGCTGCGGTCGGCGGCTCAGGAGGCTCTGGGGGGCGCAGAGCGGGGCGCTGCTG	181
OY	844	gtgcgagctgtctgcagagcgctgcggtggccaagatgcccggagtggagcgagagcctcgt	903
Db	180	GTGCGGCTGTGTCGAGGCCCCTGCGCTGGCCAGAAATGCCCGGGGCTTGAGCGGAGCGCTCCGT	121
OY	904	gagcgctctcccccctgcagctgatccgcgcgccctctatttatctcaacctctggca	963
Db	120	GAGCGCTTCTCCCTGTCGACACTGATCCGCGCCCTCTATTATTATCTACATCCCTTGCA	61
OY	964	ccccactgtcacctgaagaaggcttlltllaataagaagaatgagagttcttaaacgt	1023
Db	60	CCCCCTGTGCACTGAAAGAGGCTTTTTTTTAATATGAAGAATAGGTTTCTTAAGTT	1
RESULT	7		
LOCUS	AM662363/c		
DEFINITION	h125f01.x1 NCI-GCAP.C014 Homo sapiens CDNA clone IMAGE:2973337 3'	EST	06-APR-2000
VERSION	AM662363		
KEYWORDS	AW662363.1 GI:7454901		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
COMMENT	Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs.rem@nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: Image.liml.gov/image/html/lifresources.shtml Seq primer: -40UP from Glbpco High quality sequence stop: 368. Location/Qualifiers 1..514 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2973337" /clone_lib="NCI-CGAP.C014" /tissue_type="moderately-differentiated adenocarcinoma" /lab_host="DH10B" /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"		
BASE COUNT	113 a	156 c	159 g
ORIGIN			85 t 1 others

Query Match	46.1%	Score 496.2	DB 119	Length 514
Best Local Similarity	99.0%	Pred. No. 4.5e-93		
Matches 509	Conservative	0	Mismatches 4	Indels 1
Gaps				1

  

OY	532	ccccccgcaactgtgaagcgccttggcccttgagcccacatgtgtccaaggctcttcctcccat	591
Db	514	CCCCACAGCACTGCACGGCCCTGCGGCCCTTCATATGTGCACAGGCTCTTCTCCCAT	455
OY	592	gaacacctgtgaccacagtgcactgtgtctccctctcagaccagaaggtacacaagactgag	651
Db	454	GACACCNTGTGCACAGCTGCACTGGCTTCCCCTCAGCACACAGGATTACAGAGACTGAG	395
OY	652	gaagtgtgagcgtgccgttaatcgacttttgtgtcttccaaagatatcacaagaagctgt	711
Db	394	GAGTGTAAGCGCGCCGTCATGCATTTGTGGCTTTCACAGACATCTCCATCAAAGAGCTYG	335
OY	712	cagggcgtgtgtcgaagcccttgagagcccccgaagagcgtgtgtgtcgaacaccaaagggcggac	771
Db	334	CAGCGGCTGTCTCAGAGCCCTCGAGGCCCGGAGAGGCTGGGGTCCGACACAAGAGGCGGGCC	275
OY	772	cgcgcgaccttgacagctgaagagctgtcgcgcgcgtcacagaagctctcctggggcgacagac	831
Db	274	CGCGGGGCTTSCACACTGAAGCTGGGTGGCGGCTACAGGACTCTCTGGGGGCGCAGGAC	215
OY	832	ggggcgctgtgtgtgtgcgagctgtgtcgaagcgctgcgcgtgtgcagaagatgcccggcgtgag	891
Db	214	GGGGCGCTGTCTGCTCCGCTCTCGCAGCGCGCTGCGGTGCCAGAGATGCCGGGCTGGAG	155
OY	892	cggagacgttccgtgaagcgtctctctccctgtgtgaactgatcctgtgccccctatttatct	951
Db	154	CGGACGTCCTCGAGACGGCTCTCTCCCTGTGCATACTCTGGCCCCCTGTATTATTCT	95
OY	952	aacatccttgcgaccccaactgtcactcgaagaagac--ttttttaataagaagaatgag	1010
Db	94	ACATCCTTGGCACCCCACTTGCACTGCAAAAGAAGGCTTTTTTTTAAATAGAAATAATGAGG	35
OY	1011	ttttttaagcttattttataaagcttttcat	1044
Db	34	TTTTCTTAAAGCTTATTTTATTAAGCTTTTTCAT	1

  

RESULT	8
BE873766	697 bp mRNA EST 20-OCT-2000
LOCUS	
DEFINITION	601483915P1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886635 5', mRNA sequence.
ACCESSION	BE873766
VERSION	BE873766.1 GI:10322542
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	I (bases 1 to 697)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue Procurement: DCTD/BIP/Gasdar CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LAM9663 row: m column: 04 High quality sequence stop: 675. Location/Qualifiers 1..697 /organism="Homo sapiens" /db_xref="taxon:9606"



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/clone="IMAGE:3886635"
/clone_lib="NH_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: PCMV-SF0R6; Site: 1; Not;
Site: 2; Salt; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT      112 a      245 c      224 g      115 t      1 others
ORIGIN
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Query Match      45.3%; Score 488; DB 141; Length 697;
Best Local Similarity 92.8%; Pred. No. 2.3e-91;
Matches 567; Conservative 0; Mismatches 36; Indels 8; Gaps 5;
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OY 1 gctctccctgctccagcaagaccatgagggcgctlgagggcgagggcgtctgctgctg 60
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Db 55 GCTCTCCCTGCTCCAGCAAGACCATGAGGGCGCTGAGGGGCCAGGCGCTGCTCCTGCTG 114
|||||
OY 61 tgcctgtgtgtgagcgtgctgctgctgctgctgctgctgctgctgctgctgctgctg 120
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Db 115 TGCTGTGTGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 174
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OY 121 aacccacactacccctgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 180
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Db 175 ACACCACTACCTGCTGCGGGAGCAGACAGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 234
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OY 181 ccccgagcacttctgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 240
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Db 235 CCCCAGGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 293
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OY 241 tgcacgcgcgcacactacacgagcttctgagcagcttctgagcagcttctgagcagcag 300
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Db 294 TGTCACCGCGGCACCTACACGCACTTCTGCACTTCTGCACTTCTGCACTTCTGCACTTCTG 353
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OY 301 gtctctgagggagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 360
|||||
Db 354 GTCTCTGCGGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
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OY 361 tgcgcgtgagcagcagcgtctctgagcagcagcgtctctgagcagcagcagcagcagcagc 420
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Db 412 TGCCG-TGCCGACCGGCTTCTGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 470
|||||
OY 421 ccaacgtgagcgagcgagcttctgagcagcagcagcagcagcagcagcagcagcagcagcag 480
|||||
Db 471 CCACCTGGTGGCGGCTGATTTGCCCGGGCACCCAGCAGACAGCAGAGTGGCAGCGG 530
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OY 481 tgcggcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
|||||
Db 531 TGCCCGCCAGGCACTTCTGAGCAGAGCTCCAGCTCAAAAGAGTGGCAGAGCAGCGG- 589
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OY 541 aactgagcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600
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Db 590 -AATGACAGCGC--TGCGCTGCGCTCAATGTCAGAGTCTCTCCATGAAACCTGTG 646
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OY 601 tgcacacagctg 611
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Db 647 CACAGCTGATG 657
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RESULT 9
BF001490/c 478 bp mRNA EST 06-OCT-2000
LOCUS 7988h10.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:3313603 3'
DEFINITION similar to contains PIR5, b1 TARI repetitive element ;, mRNA
sequence.
ACCESSION BF001490
VERSION BF001490.1 GI:10701765
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 478)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,  
Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/ULN, send email to:  
infocimage.lnl.gov  
Seq primer: -40bp from Glibco  
High quality sequence stop: 419.

FEATURES  
source  
location/qualifiers

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/db\_xref="taxon:9606"  
/clone\_image="3313603"  
/clone\_lib="NCI\_CGAP\_Col6"  
/tissue\_type="colon tumor, RER+"  
/lab\_host="DH10B"  
/note="Organ: colon; Vector: p7T3D-Pac (Pharmacia) with a  
modified polylinker; Site: 1; Not 1; Site: 2; Eco RI;  
Plasmid DNA from the normalized library NCI\_CGAP\_Col6 was  
prepared, and ss circles were made in vitro. Following HAP  
hybridization, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(clonoids 1057416-1061255, and 1144584-1145311).  
Subtraction by Bento Soares and M. Fatima Bonaldo. "

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BASE COUNT      108 a      146 c      144 g      80 t
ORIGIN
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Query Match      44.4%; Score 478; DB 143; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7e-89;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 566 tcaatgagcagcgtcttcctccatgacagcctgagcagcagcagcagcagcagcagcagcagcagc 625
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Db 478 TCATATGCGCAGGCTCTTCTCCATGACACCCGCTGCAACAGCTGCACTGCTTCCGCC 419
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OY 626 tcaagcagaggttacagagagcagagaggtgagaggtgagaggtgagaggtgagaggtgagaggt 685
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Db 418 TCAGCACAGGCTACGAGAGCTGAGAGGTGAGAGGTGAGAGGTGAGAGGTGAGAGGTGAGAGGTG 359
|||||
OY 686 tcaagagacatccatcaagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 745
|||||
Db 358 TCAGGACATCTTCATCAAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 299
|||||
OY 746 gctggggtccgagacacaaaggcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 805
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Db 298 GCTGGGCTCCGACACCAAGGGGGGGCGCGGGGCTTGCAGCTGAGAGCTGCTGCGCGC 239
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OY 806 tcaagagcctctgagggcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 865
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Db 238 TCACGACACTCTTGCGGGCGCAGAGACGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 179
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OY 866 gctgagcagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 925
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Db 178 GCGTGGCCAGAGATGCGCGGCTGAGCGAGAGCGCTGAGCGAGCGCTGCTGCTGCTGCTGCTGCTG 119
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OY 926 gatccctggccctcttatctatctatctatctatctatctatctatctatctatctatctatctatctatct 985
|||||
Db 148 GATCTGGGCGCCCTCTTATTTATTTCTATCTTGGACCCCACTTGACAGTAAGAAAGAGGC 59
|||||
OY 986 ttcttttaagaagaagaatgaggttcttaagcttcttttaagcttcttttaagcttcttttaagcttctttta 1043
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[illegible][illegible]



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Db 395 AGGGTACGAGAGCTGAGAGAGTGTGACGTCGTCATGACATTTGTGTGCTTCCAGAC 336
Oy 694 atcccatcaagagctgcaagcgtctgctcaagccctcagagcccgagagcgtgaggt 753
Db 335 AT-TCCATCAAGAGCTCAGACGCGCTGCTCAGAGCCCTGAGAGCCCGAGGCGGCGCT 277
Oy 754 ccacacccaaggcgagcgagcgagcgttgcaagctgacgtgacgtgagcgtgacagag 813
Db 276 CCGACA-CAGGCGGCGCGCGCGCTTGCACCTGACGTGACGTGCGGCGCTCAGGAG 218
Oy 814 ctccgtgagcgagcagagagcgagctgctgtagcgtctgcaagcgtcgagcgtgagc 873
Db 217 CTCTGAGGCGCGCAGAGAGGCGCGCTGCTGCTGCGGCTGCTGAGCGCTGCGCGTGC 158
Oy 874 aagatgcccggcgtgagagcgagcgtgagcgtgagcgtgagcgtgagcgtgagcgt 933
Db 157 AGGATGCGCGGCTGAGAGCGAGCGCTGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTG 98
Oy 934 cccctctatctatctacactctgagcaccctgacactgacagagagcgttctt 993
Db 97 CCCCCCTATTATTATTCACATCTTGACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 38
Oy 994 aaatagaagaatgaggttcttaaa 1019
Db 37 AAATGAGAGAAATGAGGTTTCTTAA 12

RESULT 12
A1857725 445 bp mRNA EST 07-MAR-2000
LOCUS W121a08.x1 NC1-CGAP_U01 Homo sapiens cDNA clone IMAGE:2425526 3',
DEFINITION mRNA sequence.
ACCESSION A1857725
VERSION A1857725.1 GI:5511330
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 445)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnlnl.gov/dbtrp/image/image.html
Insert Length: 1138 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 418.
Location/Qualifiers
1. 445.
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/clone="IMAGE:2425526"
/clone_1bp="NCI-CGAP_U01"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; Salt:
Site_2: Notti; Cloned unidirectionally. Primer: Oligo dt.
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BASE COUNT 100 a 140 c 130 g 75 t
ORIGIN
11538-014"
Average insert size 1.75 kb. Life Technologies catalog #:
Query Match 41.3%; Score 445; DB 102; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.9e-82;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 601 tgaaccagctgacagctgctccctcagcagcagaggtaccagagctgaagatgtag 660
Db 445 TGCACAGCTGCACATGCTGCTCCCTCAGACACAGGATACAGAGACTGAGAGTGTAG 386
Oy 661 cgtacgcatcagacttgtagcttccagagacatccatcaagaagctgacagcgtg 720
Db 385 CGTGCGCTGACATCTGTGTGAGCTTTCCAGAGACATCTCCATCAAGAGCTGCAAGGCTG 326
Oy 721 ctgcaagccctcgaagcccgagaggtctgaggtctgacaccaaaggcgagcgcgagcc 780
Db 325 CTGAGAGCCCTGAGAGCCCGAGAGGCTGAGGCTCCACACAAAGGCGGCGCGCGGCC 266
Oy 781 tgcagctgagcgtgctgctgagcgtcagagctcctgagggcgagcagcgagcgtg 840
Db 265 TTGCACGTGTAAGCTGCTGCTGCGGCGCTCACGAGCTCTGCGGCGCGAGACGCGCTG 206
Oy 841 ctgtagcgtcgtcgtcagcgtcgtcgagcgtgagcagagatgccggcgtgagcgtc 900
Db 205 CTGCTCGCGCTGCTGAGAGCGCTGCGCGTGGCCAGAGATGCCGCGCTGAGCGAGCTC 146
Oy 901 cgtgagcgtctcctccctcgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtg 960
Db 145 CGTAGAGCGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 86
Oy 961 gcaaccactgacagagagagcgttctttaaataagaagaatgaggttcttaag 1020
Db 85 GCACCCACTTGCACAGGAAGGCTTTTAAATAGAGAAATGAGGTTCTTAAAG 26
Oy 1021 ctattttataaagcttttcaata 1045
Db 25 CTTATTTTATAAAGCTTTTCATA 1

RESULT 13
BE879166 551 bp mRNA EST 20-OCT-2000
LOCUS BE879166
DEFINITION 601486906r1 NIH-MGC_69 Homo sapiens cDNA clone IMAGE:3689296 5',
KEYWORDS mRNA sequence.
ACCESSION BE879166
VERSION BE879166.1 GI:10327942
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 551)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnlnl.gov
Plate: L1AM9670 row: 1 column: 01
High quality sequence stop: 546.
Location/Qualifiers
1. 551.
/organism="Homo sapiens"
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Db 159 GGATGCGCGGGCTGGAGGGGAGCGCTCGTAGCGGCTCTCCCTGTGACATGATCTGGC 100  
QY 935 ccctcttatctatctacatcccttgaccccaacttgcaacgaagaagagcttttttta 994  
Db 99 cccctcttatctatctacatcccttgaccccaacttgcaacgaagaagagcttttttta 40  
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Db 39 AATAGAGAAATGAGCTTTCTTAA 15

RESULT 15  
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LOCUS AN20499.1  
DEFINITION U1-H-R11-sef-g-12-0-U1.s1.NCI\_CGAP\_Sub3 Homo sapiens cDNA clone  
IMAGE:2720447 3, mRNA sequence.  
ACCESSION AN20499  
VERSION AN20499.1 GI:6504471  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 453)  
NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:  
NCI\_CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/ILMIL at:  
www.bio.liml.gov/bdrp/image/image.html The following repetitive  
elements were found in this cDNA sequence: 1-40,  
>AT-rich#low-complexity  
Seq primer: M13 Forward  
POLYA=yes.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Journal Comment  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:  
NCI\_CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/ILMIL at:  
www.bio.liml.gov/bdrp/image/image.html The following repetitive  
elements were found in this cDNA sequence: 1-40,  
>AT-rich#low-complexity  
Seq primer: M13 Forward  
POLYA=yes.

FEATURES  
Source

Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2720447"  
/clone\_lib="NCI\_CGAP\_Sub3"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pTZ19-3-Pac (Pharmacia) with a modified  
polylinker. Site 1: Not I; Site 2: Eco RI; The  
NCI\_CGAP\_Sub3 library is a subtracted library derived from  
the NCI\_CGAP\_Sub1 library, which is a subtracted library  
derived from B1. B1 constitutes a mixture of 21  
normalized or subtracted NCI\_CGAP libraries: NCI\_CGAP\_C04  
, NCI\_CGAP\_P122, NCI\_CGAP\_P128, NCI\_CGAP\_C010,  
NCI\_CGAP\_C016, NCI\_CGAP\_K103, NCI\_CGAP\_K102,  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: November 2, 2001, 15:03:14 ; Search time 1233.97 Seconds  
(without alignments)  
10153.307 Million cell updates/sec

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Searched: 1344157 seqs, 773874588 residues  
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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96: gb\_in4: \*  
97: gb\_pi10: \*  
98: em\_ba3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	810	100.0	1048	89	AF217794	AF217794 Homo sapi
3	810	100.0	1055	10	AX082868	AX082868 Sequence
4	810	100.0	1114	9	AX055373	AX055373 Sequence
5	810	100.0	1114	9	AX056645	AX056645 Sequence
6	810	100.0	1114	88	AF104419	AF104419 Homo sapi
7	810	100.0	1168	9	AX017828	AX017828 Sequence
8	810	100.0	1428	89	AF217793	AF217793 Homo sapi



9	810	100.0	4228	95	AB029011	Human sapi
10	808.4	99.8	5769	93	AB028244	Human sapi
11	806.8	99.6	936	10	AX093178	Sequence
12	806.8	99.6	936	10	AX091545	Sequence
13	806.8	99.6	936	10	AX098029	Sequence
14	382.8	47.3	120917	93	HS1583p15	Sequence
15	378	46.7	114793	89	AF017796	Human sapi
16	129.6	16.0	525	9	AB096131	Human sapi
17	112	13.8	2432	10	AX076604	Sequence
18	112	13.8	2432	95	AB093330	Sequence
19	110.4	13.6	1335	94	AB018834	Sequence
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22	103	12.7	1206	89	AF134187	Human sapi
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28	81	10.0	2816	8	AF149908	Gallus ga
29	78.2	9.7	380	9	AB018899S2	Human sapi
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38	68	8.4	2636	89	AK001504	Human sapi
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## ALIGNMENTS

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DEFINITION Homo sapiens tumor necrosis factor receptor homolog (TR6) mRNA,
complete cds.
ACCESSION AF134240
VERSION AF134240.1 GI:4768938
KEYWORDS
SOURCE
ORGANISM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 903)
Yu,K.Y., Kwon,B., Ni,J., Zhai,Y., Eberhart,R. and Kwon,B.S.
A newly identified member of tumor necrosis factor receptor
superfamily (TR6) suppresses LIGHT-mediated apoptosis
J. Biol. Chem. 274 (20), 13733-13736 (1999)
JOURNAL
MEDLINE
REFERENCE
AUTHORS Kwon,B.S. and Yu,K.Y.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1999) Micro/Immunol, Indiana University, 635
Barnhill Drive, Indianapolis, IN 46202, USA
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ACCESSION	AF217794
VERSION	AF217794.1 GI:6969262
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 1048)
JOURNAL	Bal,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
MEDLINE	Sandif,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
PUBLISHED	Caskey,C.T.
REFERENCE	Overexpression of M68/DCR3 in human gastrointestinal tract tumors
AUTHORS	Independent of gene amplification and its location in a four-gene
JOURNAL	cluster
FEATURES	Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
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OY	181 tgcaacgttcctctcgaggagagctgtaggagagagcaggcgttgcacgccaaccaac 240

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Db	383	CGTGCCTCCCGCTGGCGCACCGGCGCTTCTTCCGCGACGCTGGCTTCTGGTTGGACACGCA	442								
QY	301	tcgtctcacctcgtgctgacgagctatgtcccccgggacacccacagaaacagcagtg	360								
Db	443	TGCTTCCACCTGGGCGCGGTGATTTCGCCCGGGACACCCACGCCAACAACGACGATGC	502								
QY	361	cagccgtgccccccacagcacccttcacacacacacacacacacacacacacacacac	420								
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QY	601	cgcgtcgtcgc	660								
Db	743	CGGCTGCTGACAGGCGCTTGCAGAGCGCGGAGGCGTGGGCTCGACACACACACAC	802								
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QY	721	gcgcgtcgtcgc	780								
Db	863	CGGCTGCTGACAGGCGCTTGCAGAGCGCGGAGGCGTGGGCTCGACACACACACAC	922								
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ACCESSION	AX082868										
VERSION	AX082868.1	GI:13184802									
KEYWORDS											
SOURCE	human.										
ORGANISM	Homo sapiens										
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.										
JOURNAL	1 (bases 1 to 1055)										
FEATURES	Hsu, H.										
SOURCE	Ntr3, a member of the Tnf-receptor supergene family										
	Patent: WO 0110908-A 1 15-FEB-2001;										
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LOCUS AX056645  
DEFINITION Sequence 1 from Patent M0075316.  
ACCESSION AX056645  
VERSION AX056645.1 GI:12309639  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1114)  
AUTHORS Ashkenazi, A.J., Goddard, A., Gurney, A.L., Hillan, K., Napier, M. and Wood, M.I.  
TITLE Methods and compositions for inhibiting neoplastic cell growth  
JOURNAL Patent: WO 0075316-A 1 14-DEC-2000;  
Genentech, Inc. (US)  
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LOCUS AF104419  
DEFINITION Homo sapiens decoy receptor 3 (DCR3) mRNA, complete cds.  
ACCESSION AF104419  
VERSION AF104419.1 GI:4106877  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1114)  
AUTHORS Pitt, R.M., Marsters, S.A., Lawrence, D.A., Roy, M., Kischkel, F.C., Dowd, P., Huang, A., Donahue, C.J., Sherwood, S.W., Baldwin, D.T., Godowski, P.J., Wood, W.I., Gurney, A.L., Hillan, K.J., Cohen, R.L., Goddard, A.D., Botstein, D. and Ashkenazi, A.  
TITLE Direct Submission  
JOURNAL Submitted (04-NOV-1998) Molecular Oncology, Genentech, 1 DNA Way, San Francisco, CA 94080, USA  
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BASE COUNT  
ORIGIN



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LOCUS	AF217793	1428 bp	mRNA
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ACCESSION	AF217793		
KEYWORDS	AF217793.1 GI:6969260		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1428) Bai,C., Connolly,B., Metzker,M.L., Hillard,C.A., Liu,X., Caskey,C.T., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and Caskey,C.T.		
TITLE	Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)		
MEDLINE	20122600		
PUBMED	10655513		
REFERENCE	2 (bases 1 to 1428)		
AUTHORS	Bai,C.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-DEC-1999) WP26a-1000, Merck Research Laboratories, Sunneytown Pike, West Point, PA 19403, USA		
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	SVSSSECCPHRNCTALGLALNVGSSSHDTLCTSGCPPLSTRPVPAEHCERAVIDP		
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BASE COUNT	240 a	500 c	448 g
ORIGIN			240 t

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Best Local Similarity	100.0%		Pred.	No.	1,3e-127:	
Matches	810:	Conservative	0:	Mismatches	0:	Indels
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OY	181	tgcacagtcctcctctgaggagcgtatgaggaaggagacagcagcttcacagccacccacac	240
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OY	241	cgtgactcgcgctgcgcagccagcagctctcttcgcagcagctgtttcttgccttggagacgca	300
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OY	661	gcgcactcctgcagctgaaagctcgtctgcgcgcgtctcaagcagctcctctgggggtgcgagaaggg	720
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Db	1245	GGCGCTGCTGGTGGCGCTGCTSCAAGGCGCTGGCGCTGGAGATGCCCCGGGCTGGAGCGG	1304
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Db	1305	AGCGTCCGTGAGCGCTTCTCCTCCTGTGTGCAC	1334

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LOCUS	4228 bp mRNA
DEFINITION	Homo sapiens mRNA for KIAA1068 protein, partial cds.
ACCESSION	AB029011
VERSION	AB029011.1
KEYWORDS	GI:5689512
SOURCE	Homo sapiens brain cDNA to mRNA, clone_11b;pbu:ncscript11 SK plus clone:hk02589.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (sites)
TITLE	Kikuno, R., Nagase, T., Ishikawa, K., Hirosewa, M., Miyajima, N., Tanaka, A., Kotani, H., Nomura, N., and Ohnara, O.
	Prediction of the coding sequences of unidentified human genes.
	XIV. The complete sequences of 100 new cDNA clones from brain which
	code for large proteins in vitro



JOURNAL DNA Res. 6 (3), 197-205 (1999)  
 MEDLINE 93397452  
 REFERENCE 2 (bases 1 to 4228)  
 AUTHORS Ohara, O., Nagase, T., and Kikuno, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-JUN-1999) to the DDBJ/EMBL/GenBank databases. Osamu

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
(E-mail: cdna1info@kazusa.or.jp, Tel: +81-438-52-3913,  
Fax: +81-438-52-3914)

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Db	3641	CAGCGCTGCCCCCGGAGGCACTTCTCAACACAGAGCTTCAGCTCAAGCAAGTCCAGGCC	3700
QY	421	CACGCAACTGCACGCGCCTTGGCTGTGCCTCAATGTGCAAGCTCTCCCTCCATGAC	480
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LOCUS	HSMB02484
DEFINITION	Homo sapiens mRNA; cDNA DKFZp43400510 (from clone DKFZp43400510).
ACCESSION	AL157435
VERSION	AL157435.1
KEYWORDS	GI:7018508
SOURCE	
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
TITLE	1 (bases 1 to 5769)
JOURNAL	Duesterhoeft, A., Lauber, J., Mewes, H.W., Well, B. and Wiemann, S. Direct Submission Submitted (15-FEB-2000) MIPS, Am Klopfersplitz 18a, D-82152 Martinsried, GERMANY
COMMENT	Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de; sequenced by Oigen (Hilder/Germany) within the cDNA sequencing consortium of the German Genome Project.
	This clone (DKFZp43400510) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Neuberweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <a href="http://www.mips.biochem.mpg.de/proj/cdnr/">http://www.mips.biochem.mpg.de/proj/cdnr/</a> .
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## RESULT 12

AX097545 936 bp DNA PAT 30-MAR-2001  
LOCUS Sequence 3 from Patent WO0118055.  
DEFINITION AX097545  
ACCESSION AX097545  
VERSION AX097545.1 GI:13514210  
KEYWORDS  
SOURCE human

## ORGANISM

human  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 936)  
AUTHORS Atkinson,P.R., Tian,Y. and Wlitcher,D.R.  
TITLE Fluit analog compounds and formulations thereof  
JOURNAL Patent: WO 0118055-A 3 15-MAR-2001;  
ELI LILLY AND COMPANY (US)  
FEATURES  
source Location/Qualifiers

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## RESULT 13

AX098029 936 bp DNA PAT 30-MAR-2001  
LOCUS Sequence 3 from Patent WO0118202.  
DEFINITION AX098029  
ACCESSION AX098029  
VERSION AX098029.1 GI:13514890  
KEYWORDS  
SOURCE human

## ORGANISM

human  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 936)  
AUTHORS Atkinson,P.R., Tian,Y. and Wlitcher,D.R.  
TITLE Fluit analog compounds and formulations thereof  
JOURNAL Patent: WO 0118202-A 3 15-MAR-2001;  
ELI LILLY AND COMPANY (US)  
FEATURES  
source Location/Qualifiers

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Best local similarity 79.3%; Pred. No. 1; 9e-56;  
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QY 241 cgtgcctgcgcgtgc 300  
DB 695 CGTGCCTGCGCGTGCAGCGGCTTCTTGTGCGCAGCGTGTCTGTGACACACGCA 754  
QY 301 tctgttccacctcgtgtgc 333



Db 755 TCGTGTCCACTGTGTCGGCGCTGATTGCCCGGGTGAGAGTGGGCGAGGGAGGGGCC 814  
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Db 995 AGAGAGTGCAGACGCGCCAGCAGCAGCGCCGTCGGGCGCTGCGCTCAATGTGCACG 1054  
OY 465 ctctctctccatgacacacctgtgcacacagctgcagctgctccctcagcagcaggt 524  
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OY 525 accagag 532  
Db 1115 ACCAGGTG 1122

RESULT 15  
LOCUS AF217796  
DEFINITION Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and Adp-ribosylation factor related protein 1 (ARFNP1) genes, complete cds.  
ACCESSION AF217796  
VERSION AF217796.1 GI:7012928  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 114793)  
AUTHORS Bal,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X., Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and Caskey,C.T.  
TITLE Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)  
MEDLINE 20122600  
PUBMED 10655513  
REFERENCE 2 (bases 1 to 114793)  
AUTHORS Bal,C., Metzker,M.L., Liu,X. and Caskey,C.T.  
TITLE Direct Submission  
JOURNAL Submitted (20-DEC-1999) WP26A-1000, Merck Research Laboratories, Summerville Pike, West Point, PA 19403, USA  
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CDS

gene

mrna

CDS

mrna







GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 2, 2001, 13:36:20 ; Search time 76.42 Seconds  
(without alignments)  
6655.330 Million cell updates/sec

Title: US-09-006-352-1\_COPY\_115\_924  
Perfect score: 810  
Sequence: 1 gcagaacaccaccaccaccc.....agcgcttcctccgtgac 810

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues  
Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
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Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	810	100.0	813	20	AA225377 Human mFLINT #1 nu
2	810	100.0	813	21	AAA75999 DNA encoding a mat
3	810	100.0	813	21	AAA88730 Human FAS ligand i
4	810	100.0	813	21	AAA51077 Mature human FLINT
5	810	100.0	900	20	AA253575 Human FLINT #1 nuc
6	810	100.0	900	21	AA53208 Human Fas ligand i
7	810	100.0	900	21	AA51075 Human FLINT coding
8	810	100.0	903	20	AA22300 Orphan receptor (H
9	810	100.0	1055	22	AA62705 Human NTR3 nucleot
10	810	100.0	1056	21	AA53802 M68 TNF receptor r
11	810	100.0	1077	19	AAV39085 Human tumour necro

12	810	100.0	1077	21	AAA37772 Human tumour necro
13	810	100.0	1114	20	AA32744 Human DCR3 polypep
14	810	100.0	1114	21	AA58367 Human PRO212 nucle
15	810	100.0	1114	21	AA58581 Human PRO212 prote
16	810	100.0	1114	21	AA77537 Human PRO212 CDNA
17	810	100.0	1114	22	AA84421 Human PRO212 POLY
18	810	100.0	1114	22	AA91462 Human PRO212 CDNA
19	810	100.0	1164	19	AAV07654 Nucleotide sequenc
20	810	100.0	1168	20	AA209998 Human lung TNF-rec
21	810	100.0	1205	20	AAK07226 Human tumour necro
22	810	100.0	1347	21	AA63764 Human soluble TNF
23	810	100.0	1428	21	AAA53801 M68 TNF receptor r
24	810	100.0	1462	20	AA76052 Mammalian tumour n
25	808.4	99.8	825	20	AA25378 Human mature FLINT
26	808.4	99.8	825	21	AAA51078 Human FLINT #2 nuc
27	808.4	99.8	936	20	AA25376 Human FLINT #2 nuc
28	806.8	99.6	936	21	AAA88731 Human FAS ligand i
29	806.8	99.6	936	21	AAA51076 Human FLINT coding
30	806.8	99.6	936	22	AA77696 CDNA encoding huma
31	806.8	99.6	1137	21	AA92404 Monkey Fas ligand
32	727.4	89.8	900	21	AA53209 Human APO6 DNA. H
33	647	79.9	767	20	AA23419 DNA encoding a hum
34	641.2	79.2	899	20	AA89503 Human soluble TNF
35	530.4	65.5	1859	21	AA63765 Human DCR3 EST seq
36	473.4	58.4	491	20	AA32745 Human TNFR superfa
37	459	56.7	459	20	AA84621 Human TNFR soluble
38	459	56.7	459	21	AA63757 Human tumour necro
39	394.4	48.7	397	20	AAK07227 Human tumour necro
40	384.4	47.5	1667	19	AA39086 Human tumour necro
41	384.4	47.5	1667	21	AA37773 Human tumour necro
42	378	46.7	7720	21	AAA3800 Genomic DNA encodi
43	245.2	30.3	271	20	AA32747 Human DCR3 EST seq
44	242.2	29.9	283	20	AA32752 Human DCR3 EST seq
45	218.8	27.0	226	20	AA32751 Human DCR3 EST seq

# ALIGNMENTS

RESULT	1
AA225377	
ID	AA225377 standard; cDNA; 813 BP.
AC	AA225377;
XX	
DT	17-DEC-1999 (first entry)
XX	
DE	Human mFLINT #1 nucleotide sequence.
XX	
KW	Human; FLINT; mFLINT; OPC3; tumour necrosis factor receptor; FasL;
KW	apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW	sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW	reperfusion-associated injury; aplastic anaemia; differentiation;
KW	growth; myelodysplastic syndrome; pancytopenic condition;
XX	myocardial ischaemia; ss.
XX	
OS	Homo sapiens.
XX	
PN	W09950413-A2.
PD	07-OCT-1999.
XX	
PF	30-MAR-1999; 99MO-US06797.
XX	
PR	30-MAR-1998; 98US-0079856.
PR	20-MAY-1998; 98US-0086074.
PR	09-SEP-1998; 98US-0099643.
PR	17-DEC-1998; 98US-0112577.
PR	18-DEC-1998; 98US-0112703.
PR	18-DEC-1998; 98US-0112933.
PR	22-DEC-1998; 98US-0113407.
XX	
PA	(FLIL ) LILLY & CO ELI.



XX Bunnol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;  
PT Hui KY, Kharitonkov A, Mizrihi J, Ma S, Nodlitt TW, Reidy CA;  
PI Song HY, Wang J, Wu X, Zuckerman SH;  
XX WPI: 1999-591319/50.  
DR P-PSDB; AA442184.  
XX  
XX Use of mature FLINT for treating acute liver failure, inflammation,  
PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic  
PT and proinflammatory activity  
XX  
XX Claim 29; Fig 3; 99PP; English.

CC The present invention describes therapeutic applications of mature FLINT  
CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT  
CC (mFLINT), which is a member of the tumour necrosis factor receptor  
CC superfamily, is used for treating acute liver failure, inflammation of  
CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated  
CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated  
CC injury or disorder such as hypercoagulation (including use with  
CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury  
CC or disorder, type I diabetes, cancer, cell damage or damage to an  
CC innocent bystander tissue that is induced by a chemotherapeutic agent or  
CC therapeutic irradiation, treating haematopoietic progenitor cells that  
CC have been exposed to therapeutic radiation or chemotherapy, aplastic  
CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is  
CC also used for promoting the growth or differentiation of a haematopoietic  
CC progenitor cell or CD34<sup>+</sup> cell and preventing damage to a cardiac myocyte  
CC resulting from abnormal myocardial ischaemia. The present sequence  
CC encodes human mFLINT.  
XX  
XX Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Query Match	100.0%;	Score 810;	DB 20;	Length 813;
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Matches 810;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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OY	61	caatgcccccaaggaaaccttttgtagagagcgctgcgcgcgaaacagcccccaagacggt	120
Db	64	caatgcccccaaggaaaccttttgtagagagcgctgcgcgcgaaacagcccccaagacggt	123
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QY	601	cggctctgtcagagcccttcagaaagccccagaaagctgtgtagtctccagacacaaaggtcggccgc	660
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QY	781	agcgtcgcgtgagcgcctctccctcccgctgcac	810
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## RESULT

ID AAA75999 standard; DNA; 813 BP.

AC AAA75999;

DT 19-FEB-2001 (first entry)

DE DNA encoding a mature human FAS Ligand Inhibitory Protein (FLINT).  
yy

KW Human; FAS Ligand Inhibitory protein; FLINT; analogue; apoptosis; tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis

acute respiratory distress syndrome; ulcerative colitis; chronic obstructive pulmonary disease; Crohn's disease; kw

XX  
XX  
Homo sapiens

AA  
PN WO200058465-A

05-OCT-2000

20-MAR-2000; 2000WO-US06417.

PR 30-MAR-1999; 99US-0126839.

PR 21-JUN-1999; 99US-0140156.

PR 18-FEB-2000; 2000US-0183398.

PA (ELL) LILLY &amp; CO ELL

PI Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;

PI Wroblewski VJ;

DR WPI; 2000-656167/63

[illegible]

apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis, chronic obstructive pulmonary disease, emphysema, COPD, asthma, Crohn's

pt disease - .

ps Claim 3/; Page 113; 114pp; English.

CC The presequence encodes a mature human FAS ligand inhibitory  
CC protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor  
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature  
CC FLINT protein is modified to produce analogues, which have greater  
CC potency, longer in vivo half-lives, decreased aggregation, decreased







```

Db      ||| 64 cagtcgccccccagacacttctgtcagcgccgctgcgcgagacagccccacagctgt 123
OY      ||| 121 ggcctgttccacgcgcgcacataacgcagttctggaactacttggaagcgttcgcgttac 180
Db      ||| 124 ggcctgttccacgcgcgcacataacgcagttctggaactacttggaagcgttcgcgttac 183
OY      ||| 181 tgcacagtcctctcgtcgggagcgltgaaggagagcgcgggtcttcgacagccacccaac 240
Db      ||| 184 tgcacagtcctctcgtcgggagcgltgaaggagagcgcgggtcttcgacagccacccaac 243
OY      ||| 241 cgtgctcgcgtcgcgcacgcgcgtcttcctgcgcagcgcgtgttctgttgtagacagca 300
Db      ||| 244 cgtgctcgcgtcgcgcacgcgcgtcttcctgcgcagcgcgtgttctgttgtagacagca 303
OY      ||| 301 tctgttccacactgtgtcgcgcgcgtgatatgtgcgcgggagacccccagacccaagcagtc 360
Db      ||| 304 tctgttccacactgtgtcgcgcgcgtgatatgtgcgcgggagacccccagacccaagcagtc 363
OY      ||| 361 cagcgcgtgcgcgcgcgcgcacactctcagcagcagcagctcagcagcagtcagtcagcagcc 420
Db      ||| 364 cagcgcgtgcgcgcgcgcgcacactctcagcagcagcagctcagcagcagtcagtcagcagcc 423
OY      ||| 421 cagcgcgcactcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480
Db      ||| 424 cagcgcgcactcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 483
OY      ||| 481 accctgttccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 540
Db      ||| 484 accctgttccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 543
OY      ||| 541 tctgtgagcgttcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 600
Db      ||| 544 tctgtgagcgttcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 603
OY      ||| 601 cgcgtcgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 660
Db      ||| 604 cgcgtcgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 663
OY      ||| 661 ggcgcctctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 720
Db      ||| 664 ggcgcctctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 723
OY      ||| 721 ggcgcctcgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 780
Db      ||| 724 ggcgcctcgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 783
OY      ||| 781 agcgtcgcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 810
Db      ||| 784 agcgtcgcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 813

RESULT 4
AAA51077 standard; DNA: 813 BP.
XX      AAA51077;
AC      26-SEP-2000 (first entry)
DM
XX      Mature human FLINT coding sequence.
DE
XX      FLINT: osteoprotegerin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW      FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW      anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
XX      anti-inflammatory; antibacterial; immunosuppressive; ds.
XX      Homo sapiens.
OS
XX      Key Location/Qualifiers
FH      mat_peptide 1..813
FT      /*tag= a
XX

```

```

PN      WC020037094-A2.
XX
XX      29-JUN-2000.
PD
XX      21-DEC-1999; 99WO-US30734.
PF
XX      22-DEC-1998; 98US-0113407.
PR      30-MAR-1999; 99WO-US06797.
PR      20-OCT-1999; 99US-0172239.
PA      (ELIL ) LILLY & CO ELI.
XX
XX      Cohen FU, Posada JA, Wierda D;
PI
XX      WPI: 2000-475441/41.
DR
XX      P-PSDB: AAY96598.
PT
XX      use of mature FLINT for treating e.g. acute respiratory distress
PT      syndrome, ulcerative colitis or ischemic injury during organ
PT      transplantation
PS      Example 8: Fig 3A-B; 125pp; English.
XX
XX      Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis
XX      factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
XX      prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
XX      mediated apoptosis and pro-inflammatory activity. mFLINT is useful for
XX      treating acute respiratory distress syndrome, treating or inhibiting
XX      ulcerative colitis, inhibiting ischemic injury during organ
XX      transplantation or for organ preservation during transplantation. mFLINT
XX      can also be used to treat acute liver failure, inflammation of the liver,
XX      abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
XX      inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
XX      damage to a cardiac myocyte resulting from abnormal myocardial ischemia,
XX      type I diabetes, cancer, damage to an innocent bystander tissue induced
XX      by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
XX      myelodysplastic syndromes and pancytopenic conditions.
XX
XX      Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Query Match      100.0%; Score 810; DB 21; Length 813;
Best local Similarity 100.0%; Pred. No. 5,9e-145;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 ggcgaacacccacactacccttcgcccggagcagcagagagcgggtgtgtgcgc 60
Db      4 ggcgaacacccacactacccttcgcccggagcagcagagagcgggtgtgtgcgc 63
OY      61 cagtgccccccagagacacttctgtgcagcgcgctgcgcgcgcgcgcgcgcgcgcgcgcgc 120
Db      64 cagtgccccccagagacacttctgtgcagcgcgctgcgcgcgcgcgcgcgcgcgcgcgcgc 123
OY      121 ggcctgttccacgcgcgcacataacgcagttctggaactacttggaagcgttcgcgttac 180
Db      124 ggcctgttccacgcgcgcacataacgcagttctggaactacttggaagcgttcgcgttac 183
OY      181 tgcacagtcctctcgtcgggagcgltgaaggagagcgcgggtcttcgacagccacccaac 240
Db      184 tgcacagtcctctcgtcgggagcgltgaaggagagcgcgggtcttcgacagccacccaac 243
OY      241 cgtgctcgcgtcgcgcacgcgcgtcttcctgcgcagcgcgtgttctgttgtagacagca 300
Db      244 cgtgctcgcgtcgcgcacgcgcgtcttcctgcgcagcgcgtgttctgttgtagacagca 303
OY      301 tctgttccacactgtgtcgcgcgcgtgatatgtgcgcgggagacccccagacccaagcagtc 360
Db      304 tctgttccacactgtgtcgcgcgcgtgatatgtgcgcgggagacccccagacccaagcagtc 363
OY      361 cagcgcgtgcgcgcgcgcgcacactctcagcagcagcagctcagcagcagtcagtcagcagcc 420
Db      364 cagcgcgtgcgcgcgcgcgcacactctcagcagcagcagctcagcagcagtcagtcagcagcc 423

```







OY	661	gagcgcttcgaacttgaagaactcgtcgcgacgcatacagagatcccttgaggcgcaagacggg	720
Dd	751	gagcgcttcgaacttgaagtctgctcgcgacgcatacagagatcccttcggggcgcaagacggg	810
OY	721	gagccttcgttcgcgcgcgtctcgaagcgacgtcgcgatgagccaagaaatgccccggagctgagcg	780
Dd	811	gagcgtcgctggtgagcgctgctgcgaagcgctgcgcgtgagccaagaaatgcccccggagctgagcg	870
OY	781	agcgtccgtgagcgtctctctccctgtagcac	810
Dd	871	agcgtccgtgagcgtctctctccctgtagcac	900
 RESULT 6 AAA53208 ID AAA53208 standard; cDNA; 900 BP. AC XX XX AA53208; XX DT 03-JAN-2001 (first entry) DE Human Fas ligand inhibitor FLINT coding sequence. XX XX Human: Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease; KW inflammation; infectious disease; ischemia; Alzheimer's disease; KM Parkinson's disease; Crohn's disease; transplantation; ss. XX OS Homo sapiens. XX FH Key Location/Qualifiers FT CDS 1..900 FT /tag= a FT /product= "FLINT" FT /partial FT sig_peptide 1..90 FT mat_peptide 91..900 FT /*tag= b FT /*tag= c XX PN WO200034782-A1. PN PD 15-JUN-2000. XX PE 07-DEC-1999; 99WO-US28696. XX PR 09-DEC-1998; 98US-0111575. PR 09-DEC-1998; 98US-0111580. PR 07-JAN-1999; 99US-0115069. XX PA (ELIL ) LILLY & CO ELI. XX PI Rosteck PRJ, Song HY, Su EW; XX DR MPI: 2000-433379/37. XX P-PSDB: AAB03621. XX PT Novel monkey Fas ligand inhibitor polypeptides, useful for treating PT inflammatory or autoimmune disease such as rheumatoid arthritis, PT infectious diseases such as chronic hepatitis, and PT Ischaemia/Re-perfusion conditions - XX PS Example 1: Page 88-91; 101pp; English.			

The present sequence is the coding sequence of the human Fas ligand inhibitor (FLINT). The FLINT protein is involved in cell-specific apoptosis, and can be used to treat inflammatory and autoimmune diseases such as rheumatoid arthritis, inflammatory bowel disease, graft-versus-host disease, diabetes, psoriasis and Graves' disease, infectious diseases such as HIV-induced lymphopenia, fulminant viral hepatitis B/C, chronic hepatitis and cirrhosis, and H pylori-associated ulceration, ischemia and reperfusion conditions including acute myocardial infarction, acute coronary syndrome, congestive heart failure and atherosclerosis, and Alzheimer's disease, Parkinson's diseases, acute lung

CC Injury and acute respiratory distress syndrome, Crohn's disease, brain aneurysm, brain tumor, chronic glomerulonephritis, osteoporosis, aplastic anemia, myelodysplasia, ulcerative colitis, Down's syndrome, and multiple sclerosis. In addition, the gene and protein can be used to prevent apoptosis following organ transplantation.

```
Query Match      100.0%; Score 810; DB 21; Length 900;
Best Local Similarity 100.0%; Pred. No. 6e-145;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

[illegible]



AC AAAS1075;  
 DT 26-SEP-2000 (first entry)  
 XX  
 DE Human FLINT coding sequence.  
 XX  
 KW FLINT: osteoprotegerin 3; OP3; tumour necrosis factor receptor; TNFR;  
 KW FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;  
 KW anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;  
 KW anti-inflammatory; antibacterial; immunosuppressive; ds.  
 OS  
 XX Homo sapiens.  
 FH Key Location/Qualifiers  
 FH CDS 1..900  
 FT /\*tag= a  
 FT /product= FLINT  
 FT /partial  
 FT sig\_peptide 1..87  
 FT /\*tag= b  
 FT mat\_peptide 88..900  
 FT /\*tag= c  
 XX  
 PN MO200037094-A2.  
 PD 29-JUN-2000.  
 XX  
 XX 21-DEC-1999; 99WO-US30734.  
 PR 22-DEC-1998; 98US-0113407.  
 PR 30-MAR-1999; 99WO-US06797.  
 PR 20-OCT-1999; 99US-0172239.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 PI Cohen EJ, Posada JA, Wierda D;  
 DR WPI: 2000-475441/41.  
 XX P-PSDB; AAY96596.  
 XX  
 PT Use of mature FLINT for treating e.g. acute respiratory distress  
 PT syndrome, ulcerative colitis or ischemic injury during organ  
 PT transplantation  
 XX  
 XX Example 7; Fig 1A-B; 125pp; English.  
 XX  
 CC Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis  
 CC factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and  
 CC prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas  
 CC mediated apoptotic and pro-inflammatory activity. mFLINT is useful for  
 CC treating acute respiratory distress syndrome, treating or inhibiting  
 CC ulcerative colitis, inhibiting ischemic injury during organ  
 CC transplantation or for organ preservation during transplantation. mFLINT  
 CC can also be used to treat acute liver failure, inflammation of the liver,  
 CC abnormal (hepatocytic) apoptosis, sepsis, disorders associated with  
 CC inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,  
 CC damage to a cardiac myocyte resulting from abnormal myocardial ischemia,  
 CC Type I diabetes, cancer, damage to an innocent bystander tissue induced  
 CC by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,  
 CC myelodysplastic syndromes and pancytopenic conditions.  
 XX  
 SO Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

[illegible]



PF 04-AUG-1998; 98WO-US16202.  
XX  
PR 06-AUG-1997; 97US-0054869.  
XX  
PA (PROC) PROCTER & GAMBLE CO.  
PA (REGG-) REGENDRON PHARM INC.  
XX  
PI Maslakowski PJ, Morris J, Valenzuela DM;  
XX MPI: 1999-167365/14.  
DR P-PSDB: AAM95082.  
PT Novel orphan human receptor polypeptide and nucleic acid - useful as  
PT diagnostic reagents and for treatment of muscle disorders  
XX  
PS Claim 2: Page 21: 23pp: English.  
XX  
CC This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The  
CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor  
CC receptor (TNFR). Host cells transformed with a vector comprising the  
CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the  
CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the  
CC protein are useful for diagnosis and treatment of humans and animals,  
CC especially muscle disorders, as the receptor is involved in regulation of  
CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful  
CC for screening for novel binding agents, and cognate ligands, which may be  
CC used to treat disorders associated with HUMAN NTR-1 imbalance.  
XX  
SQ Sequence 903 BP; 129 A; 324 C; 305 G; 145 T; 0 other;  
  
Query Match 100.0%; Score 810; DB 20; Length 903;  
Best Local Similarity 100.0%; Pred. No. 6e-145;  
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 gcaagaacaccaccactaccctcgtcgagcagacagagagcagctgtgtcgcc 60  
DB 91 gcaagaacaccaccactaccctcgtcgagcagacagagagcagctgtgtcgcc 150  
OY 61 cagtcgccccccagcacccttctgtcagcagcgttcgcccgcagagacagccacagctgt 120  
DB 151 cagtcgccccccagcacccttctgtcagcagcgttcgcccgcagagacagccacagctgt 210  
OY 121 ggcgcgtgtcagcagcagcactacacagcagcttctggaactactctggaagcgttcgagctac 180  
DB 211 ggcgcgtgtcagcagcagcactacacagcagcttctggaactactctggaagcgttcgagctac 270  
OY 181 tgcacagctctctcgtcgagagcgttgaagagagacagagcgttcgacagccacacaaac 240  
DB 271 tgcacagctctctcgtcgagagcgttgaagagagacagagcgttcgacagccacacaaac 330  
OY 241 cgttcgctccgctcgtcgcacccgcttcctcgagcagcgttcttctgtcttgagacgca 300  
DB 331 cgttcgctccgctcgtcgcacccgcttcctcgagcagcgttcttctgtcttgagacgca 390  
OY 301 tctgtcaccactgtgtcgcgagcgttgaatgcgcgggaccccccagccagacacagcagctgc 360  
DB 391 tctgtcaccactgtgtcgcgagcgttgaatgcgcgggaccccccagccagacacagcagctgc 450  
OY 361 cagcgcgtgccccccagcagcacttctcagccagcagcagcagcagcagcagcagcagcagcagc 420  
DB 451 cagcgcgtgccccccagcagcacttctcagccagcagcagcagcagcagcagcagcagcagcagc 510  
OY 421 caccgcgaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480  
DB 511 caccgcgaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 570  
OY 481 acccgtgtcaccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540  
DB 571 acccgtgtcaccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 630  
OY 541 tctgtgagctgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600  
  
DB 631 tctgtgagctgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 690  
OY 601 cgcgtctcagc 660  
DB 691 cgcgtctcagc 750  
OY 661 ggcgcgttcagc 720  
DB 751 ggcgcgttcagc 810  
OY 721 ggcgcgttcagc 780  
DB 811 ggcgcgttcagc 870  
OY 781 agcgttcagc 840  
DB 871 agcgttcagc 900  
  
RESULT 9  
AA62705 AAF62705 standard; cDNA; 1055 BP.  
ID AAF62705;  
AC AAF62705;  
XX 02-MAY-2001 (first entry)  
DT  
DE Human NTR3 nucleotide sequence.  
DE  
XX Human: NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV;  
KW antineoplastic; immunosuppressive; antidiabetic; antiviral; antibacterial;  
KW cytostatic; neuroprotective; antiinflammatory; anorectic; vasotropic;  
KW antirheumatic; antiarthritic; cerebroprotective; tuberculostatic;  
KW gene therapy; cancer; blood disorder; brain disorder; autoimmune disease;  
KW infection; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200110908-A1.  
PD 15-FEB-2001.  
XX  
PF 02-AUG-2000; 2000WO-US21287.  
XX  
PR 04-AUG-1999; 99US-0147297.  
XX (AMGE-) AMGEN INC.  
XX Hsu H;  
XX MPI: 2001-191521/19.  
XX P-PSDB: AAB71754.  
DR New tumor necrosis factor receptor, NTR3, useful for treating cancers,  
PT stroke, anemia, obesity, rheumatoid arthritis and transplantation  
PT rejection -  
XX  
PS Claim 1: Page 128-129; 135pp: English.  
XX  
CC The present sequence encodes the tumour necrosis factor (TNF) receptor  
CC polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful  
CC for treating diseases such as acquired-immunodeficiency syndrome (AIDS),  
CC anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,  
CC diabetes mellitus, disseminated intravascular coagulopathy, erythroid  
CC sick syndrome, haemorrhagic shock, hepatitis, insulin resistance,  
CC leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia,  
CC obesity, rejection of transplanted organs, rheumatoid arthritis, septic  
CC shock syndrome, stroke, adult respiratory distress syndrome (ARDS),  
CC tuberculosis, and a number of viral diseases. The NTR3 polypeptide is  
CC useful for identifying or developing new (ant)agonists of NTR3. It may  
CC be used as an immunogen to which antibodies may be raised. NTR3 nucleic  
CC acid molecules may be useful as hybridisation probes in diagnostic assays  
CC to test, either qualitatively or quantitatively, for the presence of an



CC NTR3 DNA or corresponding RNA in mammalian tissue or bodily fluid  
CC samples.  
XX Sequence 1055 BP; 160 A; 369 C; 340 G; 186 T; 0 other;  
SQ

Query Match 100.0%; Score 810; DB 22; Length 1055;  
Best Local Similarity 100.0%; Pred. No. 6e-145;  
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 gcagaaacccacccctaccccttgccgggagcagagacagggagcgtggtgcgc 60
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DB 157 gcagaaacccacccctaccccttgccgggagcagagacagggagcgtggtgcgc 216
QY 61 caatgcccccaagcacccttgctgcagcgcgtgcgcgcgcagacagccacagcgtt 120
    |||
DB 217 cagtgcccccaagcacccttgctgcagcgcgtgcgcgcgcagacagccacagcgtt 276
QY 121 ggcgcgtgtccacgcgcgcacacacacagcttcgtgaactactgtgagcgtgcgtac 180
    |||
DB 277 ggcgcgtgtccacgcgcgcacacacacagcttcgtgaactactgtgagcgtgcgtac 336
QY 181 tgaacagctcctgcggggagcgttgagggagagcagcgttcgcacagccacacac 240
    |||
DB 337 tgaacagctcctgcggggagcgttgagggagagcagcgttcgcacagccacacac 396
QY 241 cgtgcctgcgcctgcgcgcgcacgcgccttcctgcgcacgcgtgttcctgtgagcagca 300
    |||
DB 397 cgtgcctgcgcctgcgcgcgcacgcgccttcctgcgcacgcgtgttcctgtgagcagca 456
QY 301 tctgtccacacttggtgcgcgcgtgattgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 360
    |||
DB 457 tctgtccacacttggtgcgcgcgtgattgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 516
QY 361 cagcgcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 420
    |||
DB 517 cagcgcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 576
QY 421 cagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480
    |||
DB 577 cagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 636
QY 481 accctgtgcacacagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 540
    |||
DB 637 accctgtgcacacagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 696
QY 541 tctgagcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 600
    |||
DB 697 tctgagcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 756
QY 601 cgcgcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 660
    |||
DB 757 cgcgcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 816
QY 661 gcgcgccttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttcg 720
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DB 817 gcgcgccttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttcg 876
QY 721 gcgcgccttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttcg 780
    |||
DB 877 gcgcgccttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttcg 936
QY 781 agcgtcgcgttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttc 810
    |||
DB 937 agcgtcgcgttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttcgacgttc 966
```

RESULT 10  
ID AAA53802  
XX AAA53802 standard; cDNA; 1066 BP.  
AC  
XX AAA53802;  
XX

DT 19-DEC-2000 (first entry)  
XX  
DE M68 TNF receptor related protein coding sequence.

KW M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;  
KW receptor; immune response; cell differentiation; ligand; cancer;  
KW bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;  
KW Grave's disease; idiopathic myxedema; autoimmune diabetes;  
KW thrombotic thrombocytopenic purpura; multiple sclerosis;  
KW liver diseases; autoimmune gastritis; ulcerative colitis;  
KW glomerulonephritis; pulmonary fibrosis; heart failure;  
KW atherosclerosis; aplastic anaemia; myelodysplastic syndromes;  
KW osteoporosis; Alzheimer's disease; Parkinsons disease; stroke;  
KW myocardial infarction; human; ds.

XX Homo sapiens.

PH Key Location/Qualifiers  
FT CDS 53..95  
FT /\*tag= a  
FT /product= M68 polypeptide

XX MO200046247-A1.

XX 10-AUG-2000.

XX 04-FEB-2000; 2000MO-US03037.

XX 05-FEB-1999; 99US-0118902.

XX 20-DEC-1999; 99US-0172754.

XX (MER1 ) MERCK & CO INC.

XX Bai C;

XX WPI; 2000-506066/45.

XX P-PSDB; AAY97246.

XX Isolated human M68 nucleic acids and proteins which are part of the

XX tumor necrosis factor receptor (TNFR) family; useful for identifying

XX modulators that may be used to treat various diseases e.g. cancer,

XX osteoporosis, Alzheimer's disease

XX Claim 21; Page 73-75; 80pp; English.

XX The M68 protein is a member of a family of proteins which have

XX roles in immune responses, cell death, cell proliferation and

XX stimulation of cell differentiation. M68 lacks a transmembrane domain

XX and is a secreted factor suggesting that it functions as a natural

XX inhibitor for its ligand. The altered expression pattern of M68 in a

XX multitude of tissues suggests that M68 may play a role in cancer by

XX binding to its ligand and blocking apoptotic cell death induced by

XX such a ligand. This anti-apoptotic role of M68 suggests that

XX modulators of M68 will be useful in treatment of apoptosis-related

XX diseases such as various forms of cancer and various bone disorders.

XX M68 nucleic acids and proteins are therefore useful for treating

XX conditions involving atypical apoptosis and for identifying

XX modulators of M68. Modulators of M68 are useful for treatment of

XX cancer and other diseases associated with abnormal levels of

XX apoptosis including systemic lupus erythematosus, Hashimoto's

XX thyroiditis, Grave's disease, idiopathic myxedema, autoimmune

XX diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,

XX liver diseases, autoimmune gastritis, ulcerative colitis,

XX glomerulonephritis, pulmonary fibrosis, heart failure,

XX atherosclerosis, aplastic anaemia, myelodysplastic syndromes,

XX osteoporosis, Alzheimer's disease, Parkinsons disease, stroke, and

XX myocardial infarction.

SQ Sequence 1066 BP; 178 A; 367 C; 335 G; 186 T; 0 other;

Query Match 100.0%; Score 810; DB 21; Length 1066;  
Best Local Similarity 100.0%; Pred. No. 6e-145;







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Qy	361	cagccgcgtgacccccccagagcacactctctccagccagacagctctcaagctctcaagagcagctgtgcacgcc	420
Db	475	cagccgcgtgacccccccagagcacactctctccagccagacagctctcaagctctcaagagcagctgtgcacgcc	534
Qy	421	caaccgcgaactctgacacgagccctctgggacccctctgagccctcaatgtgtgcacagagctctctccctccatgac	480
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Qy	481	accctctgtgacacacagctctgacatctgtgctcttccccctcaagccacaggggtaccagagagctctgagagag	540
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Qy	661	gcggcactctgcagactctgaagactctgtgtctcagtcagggctccacagggagctctctctgtgggtgcagagacgggt	720
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XX	AAA37772;	
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XX		
Human	tumour necrosis factor receptor-6 alpha coding sequence.	
KM	Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;	
KM	ocular neovascularisation; solid tumour; malignancy; prostate cancer;	
KM	breast cancer; colon cancer; diabetic retinopathy; microbial infection;	
KM	pre-maturity macular degeneration; allergy; inflammation; tissue damage;	
KM	thyroid associated opthalmopathy; cell damage; parasitic infection;	
KM	bone disease; osteoporosis; atherosclerosis; cardiovascular disease;	
KW	neurodegenerative disorder; Alzheimer's disease; immune disorder;	
KW	graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;	
KW	pneumonia; septic shock; ulcerative colitis; therapy; ds.	
OS		
Homio sapiens.		
Key	Location/Qualifiers	
CDS	25..927	
FH	/**tag= a	
FT	/product= TNFR-6alpha	
ET		
XX		
MO200052028-A1.		
XX		
08-SEP-2000.		
PD		
XX		
PF	03-MAR-2000; 200OMO-US05686.	
XX		
PR	04-MAR-1999; 99US-0121774.	
PR	12-MAR-1999; 99US-0124092.	
PR	27-APR-1999; 99US-0131279.	

PR 30-APR-1999; 99US-0131964.  
PR 02-AUG-1999; 99US-0145371.  
PR 01-DEC-1999; 99US-0168235.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Gentz RL, Ni J, Ebner R, Yu G, Ruben SM, Feng P,  
XX  
XX MPI: 2000-572174/53.  
DR P-PSDB: AAY90357.  
XX  
XX Nucleic acids encoding human tumour necrosis factor receptor (TNFR)  
PT proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.  
PT Alzheimer's disease, osteoporosis and graft rejection -  
XX  
XX Claim 2; Fig 1; 332pp; English.

CC This sequence encodes the human tumour necrosis factor receptor 6  
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA  
CC and protein sequences can be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate TNFR expression. The  
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against  
CC them may be used for the treatment of a range of conditions such as  
CC disorders associated with neovascularisation (especially ocular  
CC neovascularisation) (such as solid tumours and malignancies (e.g.  
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy  
CC and pre-maturity macular degeneration), allergies, inflammation,  
CC thyroid associated ophthalmopathy tissue/cell damage, wounds, microbial  
CC and parasitic infections, bone disease (e.g. osteoporosis),  
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),  
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune  
CC disorders (e.g. graft rejection), rheumatism, liver disease,  
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative  
CC colitis.

[illegible]







RESULT 14  
AAC58367  
ID AAC58367 standard; cDNA; 1114 BP.  
XX  
XX AAC58367;  
XX  
XX 29-JAN-2001 (first entry)  
XX  
DE Human PRO212 nucleotide sequence SEQ ID NO:1.  
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
KW immunoprotective; antiinflammatory; immunosuppressive;  
KW immunostimulant; antiangiogenic; leukemia; lymphoid malignancy;  
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
KW hypothalamic disorder; glandular disorder; macrophagal disorder;  
KW epithelial disorder; stromal disorder; blastocoealic disorder;  
KW inflammatory disorder; immunologic disorder; ss.  
XX  
XX Homo sapiens.  
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XX  
XX WO200053755-A2.  
XX  
XX 14-SEP-2000.  
XX  
XX 06-JAN-2000; 2000WO-US00376.  
XX  
XX 08-MAR-1999; 99NO-US05028.  
XX 02-JUN-1999; 99WO-US12252.  
XX 23-JUN-1999; 99US-0141037.  
XX 07-JUL-1999; 99US-0143048.  
XX 26-JUL-1999; 99US-0145698.  
XX 30-NOV-1999; 99WO-US28313.  
XX 20-DEC-1999; 99NO-US30911.  
XX 05-JAN-2000; 2000WO-US00219.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
PI Watanabe CK, Wood WI;  
XX  
XX WPI: 2000-572270/53.  
XX  
XX P-PSDB: AAB24057.  
XX  
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
XX treatment, diagnosis and prevention of cancer -  
XX  
XX Claim 50; Fig 1; 286pp; English.  
XX  
XX The present invention describes an isolated antibody that binds to  
XX one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,  
XX PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
XX PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
XX PRO1187, PRO1281, PRO23, PRO29, PRO834, PRO1317, PRO1710, PRO2094,  
XX PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
XX growth. The PRO polypeptides and nucleotides are useful in the  
XX treatment, diagnosis and prevention of cancer. The antibodies and other  
XX anti-tumour compounds may be used to treat various conditions, including  
XX those characterised by overexpression and/or activation of the amplified  
XX PRO genes. Exemplary conditions or disorders to be treated with such  
XX antibodies and other compounds include benign or malignant tumours  
XX (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
XX colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
XX carcinosmas, sarcomas, glioblastomas, and various head and neck tumours),  
XX leukaemias and lymphoid malignancies, other disorders such as neuronal,  
XX glial, astrocytal, hypothalamic and other glandular, macrophagal,  
XX epithelial, stromal and blastocoealic disorders, and inflammatory,  
XX angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
XX primers and hybridisation probes used in the isolation of the human PRO  
XX sequences. AAC5367 to AAC58396 and AAB24057 to AAB24089 represent human  
XX PRO polynucleotide and protein sequences given in the exemplification of







Db 731 tgltagcgtgcggtcgcgtacgcacttctgtgcttccagagacatctccatcaagaagctgcag 790  
QY 601 cggctgctgcagggccctcgagagcccgagagggctgggttcgacacccaaggcgggccgc 660  
|||||  
Db 791 cggctgctgcagggccctcgagagcccgagagggctgggttcgacacccaaggcgggccgc 850  
QY 661 gcgaccttgcaagctgaagctgcgtcgagcggtcaagagctccttgaggcgcaagacggg 720  
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Db 851 gcgaccttgcaagctgaagctgcgtcgagcggtcaagagctccttgaggcgcaagacggg 910  
QY 721 gcgctgctggtcggagctgcgcagcggtgcgcgtggccagagatggccgggcttggaagcgg 780  
|||||  
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Search completed: November 2, 2001, 15:05:24  
Job time: 5344 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2001, 14:44:00 ; Search time 1010.9 Seconds  
(without alignments)  
7574.252 Million cell updates/sec

Title: us-09-006-352-1\_COPY\_115\_924  
Perfect score: 810  
Sequence: 1 gcagaaacacccaccacc.....agcgctccctccctgtgcac 810

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 segs, 4726426750 residues  
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	594	73.3	617	141 BE878908	BE878908 601492609
2	577	71.2	679	141 BE878006	BE878006 601489784
3	496.8	61.3	874	147 BF339551	BF339551 602039016
4	482.6	59.6	692	111 AM083241	AM083241 xc07a04.x
5	466.8	57.6	600	113 AM262121	AM262121 xq31d04.x
6	421.6	52.0	551	141 BE879166	BE879166 601486906
7	411.6	50.8	540	116 AM471440	AM471440 xw59e06.x
8	388	47.9	554	116 AM464298	AM464298 BP230015A
9	387.2	47.8	514	119 AM662363	AM662363 h125f01.x
10	381.4	47.1	475	24 AT1718743	AT1718743 as95h04.x
11	374	46.2	697	141 BE873766	BE873766 601483915
12	359	44.3	478	143 BF001490	BF001490 7988h10.x
13	354	43.7	515	111 AM083914	AM083914 xc25902.x
14	345.2	42.6	459	110 AM014771	AM014771 UI-H-B10-
15	324	40.0	445	102 AT1857725	AT1857725 w121a08.x
16	311.8	38.5	453	113 AM204999	AM204999 UI-H-B11-
17	308.8	38.1	467	1 AA025673	AA025673 z99h09.s
18	308	38.0	436	18 AT290210	AT290210 q179912.x
19	305	37.7	452	120 AM771720	AM771720 h171a02.x
20	300	37.0	430	22 AT1561219	AT1561219 tq27c11.x
21	286	35.3	468	120 AM769220	AM769220 h154h07.x
22	282.4	34.9	340	114 AM316995	AM316995 xxi0e06.x
23	281.8	34.8	417	110 AM006931	AM006931 wt08b06.x
24	280	34.6	405	21 AT520716	AT520716 tl06f10.x
25	279	34.4	359	111 AM080544	AM080544 xc33a03.x
26	271.2	33.5	295	120 AM801019	AM801019 MR3-DM06
27	267.4	33.0	388	151 BF591174	BF591174 7h54h12.x
28	260.6	32.2	428	3 AA155701	AA155701 z070e05.x
29	253.4	31.3	358	111 AM080904	AM080904 xc21f07.x
30	251	31.0	406	22 AT1624643	AT1624643 ts43a12.x
31	250.2	30.9	344	17 AT1185297	AT1185297 qe36c02.s
32	242.2	29.9	283	3 AA155646	AA155646 z070e05.s
33	239.4	29.6	461	11 AA740147	AA740147 ob26a08.s
34	237	29.3	358	18 AT182851	AT182851 q78a09.x
35	227.4	28.1	378	9 AA613366	AA613366 nq31a08.s
36	218.6	27.0	423	111 AM083605	AM083605 xc19h07.x
37	198	24.4	333	122 AM955349	AM955349 EST367419
38	195	24.1	211	102 AT1862475	AT1862475 td16h06.x
39	183	22.6	233	1 AA025672	AA025672 z99h09.r
40	181	22.3	378	19 AT180034	AT180034 tq19e10.x
41	179	22.1	191	5 AA325843	AA325843 EST28933
42	178	22.0	271	114 BE871829	BE871829 601489305
43	166.2	20.5	413	114 AM272130	AM272130 xul0h06.x
44	160.6	19.8	544	104 AT1980373	AT1980373 pat.pk002
45	160	19.8	273	103 AT1910466	AT1910466 w131d03.x

## ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	BE878908	BE878908 617 bp mRNA	EST	20-OCT-2000								
		601492609	NIH_MGC_69	Homo sapiens	CDNA clone	IMAGE:3894794.5						
		BE878908	BE878908	BE878908.1	GI:10327684							
		human.										
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
		Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.										
		NIH-MGC http://mgi.nci.nih.gov/										
		National Institutes of Health, Mammalian Gene Collection (MGC)										
		Unpublished (1999)										
		Contact: Robert Strausberg, Ph.D.										

Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTF/gazdar  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://lmage.llnl.gov  
Plate: LAM9685 row: a column: 03  
High quality sequence stop: 617.  
Location/Qualifiers

## FEATURES

Source  
1. 617  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3894794"  
/clone.lib="NIH\_MGC\_69"  
/tissue\_type="large cell carcinoma, undifferentiated"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: pCMV-Sp0R6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."

## BASE COUNT

91 a 224 c 203 g 99 t

## ORIGIN

Query Match 73.3%; Score 594; DB 141; Length 617;  
Best local Similarity 99.8%; Pred. No. 1,9e-111;  
Matches 605; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

153 ctggaactactctgagcgctcgtcgtctactgcaacgtctctgaggagcgltagagga 212  
3 CTGGAACCTACTCTGAGCGCTGCGGCTACTGCAACGTCCTGCGGGAGCGTAGAGA 62  
213 ggcagcggtctgcaacgcaaccccaacgctgctgcgctgcgcagcggtcttcgc 212  
63 GGCAGCGGCTTGTGCTTGGAGCAGCAGCTGCTGCGGCTGCGGCTGCTTTCGC 122  
273 ggcagcggtctgctgctgtagcagcagcagctgctcagcggtgagcggtgagc 332  
123 GCACGCTGCTTGTGCTTGGAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 182  
333 ggcagccccagcagcaacagcagcagcagcagcagcagcagcagcagcagcag 392  
183 GGCAGCCCCAGCAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 242  
393 cagctcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 452  
243 CAGCTCAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 302  
453 caatgtgcaagcgtctcctccatgacacccctgtgacagcagcagcagcagcagc 512  
303 CAATGTGCCAGGCTCTTCTCCATGACACCTGTGTGACACGCTGCTGCTGCTGCT 362  
513 cagcaccaggtacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 572  
363 CAGCACCAGGCTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 422  
573 ccagagacatccataaagagcgtcagcgctgctgtagcagcagcagcagcagcag 632  
423 CCAGGACATCTCATCAAGAGGCTGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTG 482  
633 ctgggtgtccagacacagcagcagcagcagcagcagcagcagcagcagcagcagc 692  
483 CTGGGTGTCCAGACACAGGCGGGCGCGCGCGCTGTGACATGAGCTGCTGCGGCT 542  
693 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 752  
543 CAGCAGAGCTCTGCGGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 601  
753 cgtgagc 758  
602 CGTGGC 607



RESULT	2
LOCUS	BE878006
DEFINITION	BE878006 679 bp mRNA EST 20-OCT-2000 601849784F1 NH_MGC_69 Homo sapiens cDNA clone IMAGE:3891908 5', mRNA sequence.
ACCESSION	BE878006
VERSION	EST.
KEYWORDS	GI:10326782
SOURCE	human. tissue: human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 679)
AUTHORS	NH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	

Plate: L1AM9677 row: h column: 21  
High quality sequence stop: 672.  
Location/Qualifiers

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source
1. 6/79
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGF:3891908"
/clone_1fp="NH.MCC.69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="PH10B (phage-resistant)"
/notes="Organ: lung; Vector: pCMV-SPE0T6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.1 Kb. Library constructed by Life
Technologies."
113 a 239 c 204 g 123 t
BASE COUNT
ORIGIN

```

[illegible][illegible]

RESULT	3				
BF339551					
LOCUS	BF339551	874 bp	mRNA	EST	22-NOV-2000
DEFINITION	60203010F1 NCI_CGAP_Brn64 Homo sapiens	CDNA	clone IMAGE:4186995		
ACCESSION	BF339551				
VERSION	BF339551.1	GI:11286006			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 874)
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: David N. Louis, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Place: LLM5508 row: p column: 04 High quality sequence stop: 701. Location/Qualifiers
FEATURES	

FEATURES	source	Location/Qualifiers
1	874	/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="IMAGE:4186995"
		/clone_1lb="NCI CGAP_Brn64"
		/tissue_type="fibroblastoma with EGR amplification"
		/lab_host="DH10B (TI phage-resistant)"
		/note="Osgar: Brain; Vector: pCMV-Sport6; Site: 1; Note: Site: Salt; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
BASE COUNT	129 a	299 c
ORIGIN	301 g	145 t
Query Match	61.3%	Score 496.8; DB 147; Length 874;
Best Local Similarity	87.7%;	Prod. No. 1.2e-91;
Matches 365; Conservative	0;	Mismatches 77; Indels 2; Gaps 2.
QY	1	gcgaagaaccaccactcaccctgctggagagcagagagagagagcgcgtgtgtgcgc 60
Db	188	gcgagaaacacccaccttaccctctggcggagacacaaagacagggagggcgtgctgtggcc 247
QY	61	cagtgccccccagagcaccttctgtcagcgcgcctgtgccgcagagacagcccccaagcgtgt 120
Db	248	caatgtcccccacagacacattttgtgcacagcggccgtggccgcgaacacagcccccacacacgtgt 307
QY	121	gagccctgttcacacgcgcacactacacagactcttgaaactaccttgagagctgcgcgtac 180



```
Db 308 GGGCCGCTGTCACCGCCGCTACACGCACTTCTGGAGACTGAGCGCTGCCGCTAC 367
Qy 181 tgcacgtctcttgcgagagagcgtgagagagagcagagagcttgcacagccacacac 240
Db 368 TGCAGACTCTCTGCGGGGAGCGTGAGAGAGAGGAGGAGGCTTGCACGCGCACACAC 427
Qy 241 cgtgctgcgctgcgagcagcgtcttgcgagcagcgtgcttgcgagcagcagc 300
Db 428 CGTGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCA 487
Qy 301 tctgttcacactgtgtgcgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 360
Db 488 TCGGTGTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
Qy 361 cagcgcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 420
Db 548 CAGCGTGCCTCCCGGAGCACTTCTGAGCAGCAGCTGCAAGCTGCAAGCTGCAAGCTG 607
Qy 421 cagcgcagctgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480
Db 608 CACCG-AACTGACAGCGCTGCGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 666
Qy 481 accctgtgcacacagctgcagctgtcttccctcagcagcagcagcagcagcagcag 540
Db 667 ACCCTGTGACACAGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725
Qy 541 tctgagcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 600
Db 726 TGTGAGCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 785
Qy 601 cgcgtgcgtgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 644
Db 786 GTGTGGGCTTGAAGCCGAGAGGTGGGTGCGCGCAGGGGGGCGCG 829
```

```
RESULT 4
LOCUS AW083241/c
DEFINITION x07604.x1 NCI-CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583534.3'
similar to TR:095407 095407 DECOY RECEPTOR 3.; contains 11 bp MER22
repetitive element;; mRNA sequence.
ACCESSION AM083241
VERSION AM083241.1 GI:6038393
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 692)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bdnp/image/image.html
Seq primer: -40UP from Glibco
High quality sequence stop: 414.
FEATURES
source
1..692
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2583534"
/clone_1lb="NCI-CGAP_Co21"
/tissue_type="moderately differentiated adenocarcinoma"
```

```
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Normalized to cot >500. Average insert size 1.04kb.
Library constructed by Life Technologies."
BASE COUNT 136 a 205 c 235 g 115 t 1 others
ORIGIN
```

```
Query Match 59.6%; Score 482.6; DB 111; Length 692;
Best Local Similarity 97.7%; Pred. No. 9; Se-89;
Matches 510; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
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```
Qy 290 tgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 349
Db 619 TGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 561
Qy 350 acacgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 409
Db 560 ACACGAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 501
Qy 410 agtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 469
Db 500 AGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 441
Qy 470 cctccatgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 529
Db 440 CTTCATGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 381
Qy 530 gacgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 589
Db 380 GAGCTGAGAGATGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 321
Qy 590 agagcgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 649
Db 320 AGAGCCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 261
Qy 650 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 708
Db 260 GGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 201
Qy 709 gcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 768
Db 200 GCGCAGAGCAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 141
Qy 769 ggcgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 810
Db 140 GGGCTGAGCGAGCGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 99
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```
RESULT 5
LOCUS AM262121/c
DEFINITION xq31004.x1 NCI-CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752231.3'
similar to TR:095407 095407 DECOY RECEPTOR 3.; contains 781 bp
TARI repetitive element;; mRNA sequence.
ACCESSION AM262121
VERSION AM262121.1 GI:6638937
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 600)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
```



















COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, send email to: info@image.llnl.gov  
Seq primer: -400P from Glibco  
High quality sequence stop: 419.

FEATURES  
source  
1. 478  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lib="NCI-CGAP-Co16"  
/tissue\_type="colon tumor, RER"  
/lab\_host="DH10B"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Co10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1057416-1061255, and 114584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 108 a 146 c 144 g 80 t  
ORIGIN

Query Match 44.3%; Score 359; DB 143; Length 478;  
Best Local Similarity 100.0%; Pred. No. 1.4e-63;  
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 452 tcaatgtccagagctctctccacgacacccctgacagagctgacgctccccc 511  
DB 478 TCAATGTCCAGAGCTTCTCTCCATGACACCCCTGACAGCTGAGCTGGCTCCCC 419

OY 512 tcaagaccagaggtacacagagctgagagctgagcgtgacgctgacgctgagct 571  
DB 418 TCAGCACCAGGATACGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTT 359

OY 572 tccagagacatcgcataaagagctgacgagctgacgagctgacgagctgagag 631  
DB 358 TCAGAGACATCTCCATMAAGAGCTGACGAGCTGCTGAGAGCTGAGAGCTG 299

OY 632 gctggggtccgacacagagcgagcgagctgacgctgacgctgacgctgacgagc 691  
DB 298 GCTGGGGTCCGACACAGAGCGGCGGCGGCTTCAGCTGAGAGCTGAGAGCTG 239

OY 692 tcaagagctctcggggcgagagcgagcgagctgagctgagctgagcgagcgagc 751  
DB 238 TCAGGAGCTCTGggggcgagagcgagcgagctgagctgagctgagcgagcgagc 179

OY 752 gctggggtccgacacagagcgagcgagctgagcgagctgagcgagctgagcgagc 810  
DB 178 GCTGGGTCAGAGATCCCGGCGCTGAGAGCGAGAGCTGAGAGCTGAGAGCTG 120

RESULT 13  
LOCUS AM083914 515 bp mRNA EST 14-OCT-1999  
DEFINITION xc25902.x1 NCI-CGAP-Co19 Homo sapiens cDNA clone IMAGE:2585330 3'  
ACCESSION AM083914  
VERSION AM083914.1 GI:6039066  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 515)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, at: www.bio.llnl.gov/biopr/image/image.html  
Seq primer: -400P from Glibco  
High quality sequence stop: 355.

FEATURES  
source  
1. 515  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lib="NCI-CGAP-Co19"  
/tissue\_type="moderately differentiated adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: colon; Vector: pCMV-Sport6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Normalized to Cot 50. Average insert size 1.32kb. Normalized version of NCI-CGAP-Co18. Library constructed by Life Technologies."

BASE COUNT 102 a 160 c 158 g 94 t 1 others  
ORIGIN

Query Match 43.7%; Score 354; DB 111; Length 515;  
Best Local Similarity 94.4%; Pred. No. 1.5e-62;  
Matches 388; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

OY 400 agctcagagcgagtcgagccacacgagacgtgagcgtgagcgtgagcgtgagcgtg 459  
DB 515 AGCTCAGAGCAGAGTCCAGACCCCGCAANTGCGGAGCTGGAGCTGAGAGT 456

OY 460 ccaagctctctccatgagacacccgtagcagcagctgagctgagctgagcagc 519  
DB 455 CCAAGCTCTCTCCCATGAGACCCCTGTGACCAAGTGCAGCTGAGCTGAGCTG 396

OY 520 aggttaccagagagctgagagtgtagcgtagcgtgacgtgagctgagctgagcag 579  
DB 395 AGGTACACAGAGCTGAGAGTGTGAGCGGCTGATGACTTTGTGCTTCACAGAC 336

OY 580 atctccatcaagagctgagcagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 639  
DB 335 AT-TCATATCAAGAGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAG 277

OY 640 ccgaacacaaagcgagcgagcgagcgtgagcgtgagcgtgagcgtgagcgtgagcag 699  
DB 276 CCAGACA-CAAGGCGGCGCGCGGCTTGCAGCTGAGAGCTGCGGCGGCTGAGAG 218

OY 700 ctccctggagcgagcgagcgagcgagcgtgagcgtgagcgtgagcgtgagcgtgagc 759  
DB 217 CTCCTGGGGGCGAGAGCGGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 158

OY 760 aggatgcccgagcgtgagcgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtg 810  
DB 157 AGGATGCCCGGCGGCTGAGCGGAGAGCTGCGGAGCGCTTCTCCGTGAGAC 107

RESULT 14  
LOCUS AM014771 459 bp mRNA EST 10-SEP-1999  
DEFINITION UT-H-B10-aag-g-04-0-UI.s1 NCI-CGAP-Sub1 Homo sapiens cDNA clone  
IMAGE:2709294 3', mRNA sequence.



ACCESSION AW014771 GI:5863528  
VERSION AW014771.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 459)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA library preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
www.bio.lnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward  
POLA=yes

## FEATURES

source Location/Qualifiers

1..459  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2709294"  
/clone\_lib="NCI-CGAP\_Sub1"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pTT3D-Pac (Pharmacia) with a modified  
polylinker. Site\_1: Not I; Site\_2: Eco RI; The  
NCI-CGAP Sub1 library is a subtracted library derived from  
B1. B1 constitutes a mixture of 21 normalized or  
subtracted NCI-CGAP libraries: NCI-CGAP\_C04,  
NCI-CGAP\_Pr22, NCI-CGAP\_Pr28, NCI-CGAP\_C010, NCI-CGAP\_C016,  
NCI-CGAP\_Kid5, NCI-CGAP\_Kid12, NCI-CGAP\_Kid3,  
NCI-CGAP\_Kid11, NCI-CGAP\_Lym2, NCI-CGAP\_Pr23, NCI-CGAP\_C08,  
NCI-CGAP\_C011, NCI-CGAP\_Le12, NCI-CGAP\_Brn23, NCI-CGAP\_Lu5,  
NCI-CGAP\_Lu24, NCI-CGAP\_Lu19, NCI-CGAP\_G04, NCI-CGAP\_G06,  
NCI-CGAP\_Brn25. These 21 libraries were pooled and a  
single-stranded DNA preparation of the resulting mixture  
was used as a tracer in a subtractive hybridization with a  
driver whose composition is detailed below: NCI-CGAP\_Kid3  
pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE  
CloneIDs 1322376-1323911, 1456008-1456755, 1500552-1502855  
); NCI-CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725,  
3776-3778 (IMAGE CloneIDs 132912-132851,  
147168-1472903, 1492104-1493253) NCI-CGAP\_Lu5 pool 1 LLAM  
3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,  
1520904-1522439) NCI-CGAP\_G04 pool 1 LLAM 3164-3167,  
3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,  
1469064-1470983, 1475592-1476743) NCI-CGAP\_Pr22 pool 1  
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs  
985608-986759, 1101192-1101959, 1217928-1220615)  
NCI-CGAP\_C010 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE  
CloneIDs 1057416-1061255, 1144584-1145351) The resulting  
subtracted library contained 530,000 recombinants.  
Subtraction was performed as previously described [Bonald  
& Soares (1996): Normalization and Subtraction:  
Two Approaches To Facilitate Gene Discovery. Genome  
Research 6, 791-806.  
TAG\_LIB=NCI-CGAP\_C04  
TAG\_TISSUE=Colon  
TAG\_SEQ=CTTGC

BASE COUNT 93 a 143 c 136 g 87 t  
ORIGIN

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Matches 347; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 461 cagctcttcctccatgacacccctgtgacacgagctgactggctccctcaagacaa 520  
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Db 459 CAGGCTTCTCTCCCATGACACCCCTGTGCACAGCTGCACTGGCTTCCCTCAGACCA 400  
QY 521 ggttaccagagctgaggtgtgtgagcgtgtccgtatcgaactttgtggtcttccagaca 580  
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Db 399 GGGTACCAGAGGCTGAGGATGTGAGCGTACCTCATGACCTTGTGGCTTCCAGACA 340  
QY 581 tcccatcaagaagctgcgaacgagctgtcgtcaggccctcagagcccggaagcttgagtc 640  
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Db 339 TCTCCATCAAGAGGCTGACAGCGGTCTCTCTCAGAGCCCTCAGAGCCCGAGAGCTGGGTC 280  
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Db 279 CGACACCAAGCGCGGCGCGCGCTTGCAGCTGAAGCTGCGTGGGCGGCTCAGAGC 220  
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Db 219 TCTTGGGGGCGCAGGAGCGGGCGCTGTGTGGCTGTGAGGCGCTCGGTGGCCA 160  
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RESULT 15  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 445)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA library Preparation: Life Technologies, Inc.  
cDNA library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.lnl.gov/bbrp/image/image.html  
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High quality sequence stop: 418.

## FEATURES

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11538-014"

BASE COUNT 100 a 140 c 130 g 75 t  
ORIGIN

Query Match 40.0%; Score 324; DB 102; Length 445;



Best Local Similarity 100.0%; Pred. NO. 2e-56;  
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